

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 198439

TO: Ginny Portper

Location: REM-3C18

Art Unit: 1645

Friday, August 11, 2006

Case Serial Number: 09/904994

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

Examiner Portner,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist REM-1A65 571-272-2527



Schulwitz, Paul

From:

Portner, Ginny

Sent:

Friday, August 04, 2006 11:32 AM

To:

Schulwitz, Paul

Subject:

09/904994 nucleic and amino acid sequence search with specific gap values; claims attached

Importance: High

Thanks for your help with this search issue. I am sending the claims to you now (Snagit training WORKed!!!!!!!!) Once I check the Spec for a program name etc I will send you another email. ginny

Ginny Portner Remsen Building Art Unit 1645 Room E03, B02; Mail Box 3C18 (571) 272-0862

Claims:

34

Schulwitz, Paul

From:

Portner, Ginny

Sent:

Friday, August 04, 2006 11:44 AM

To:

Schulwitz, Paul

Subject:

FW: 09/904994 nucleic and amino acid sequence search with specific gap values; claims

attached

Importance: High

Paul, From the Specification, I found that they sued a computer program called "Align Plus for Windows, available from Scientific and Educational Software, P.O. Box 72045, Durham, NC 27722-2045 USA. I hope that this information helps. ginny

Ginny Portner Remsen Building Art Unit 1645 Room E03, B02; Mail Box 3C18 (571) 272-0862

----Original Message-----From: Portner, Ginny

Sent: Friday, August 04, 2006 11:32 AM

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Ginny Portner
Remsen Building
Art Unit 1645
Room E03, B02; Mail Box 3C18
(571) 272-0862

Schulwitz, Paul

From:

Portner, Ginny

Sent:

Friday, August 04, 2006 12:05 PM

To:

Schulwitz, Paul

Subject:

FW: 09/904994 nucleic and amino acid sequence search with specific gap values; claims

attached

Importance: High

Paul, After looking at all of the claims, I found that they claims SEQ ID Nos 1, 2 and 3. with the nucleic acid perameters of claim 23 previously emailed, and the polypeptide sequences with a different set of perameters as set forth in emailed claim 34. Thanks!!!

Ginny Portner Remsen Building Art Unit 1645

Room E03, B02; Mail Box 3C18

(571) 272-0862

-----Original Message-----From: Portner, Ginny

Sent: Friday, August 04, 2006 11:44 AM

To: Subject: FW: 09/904994 nucleic and amino acid sequence search with specific gap values; claims attached

Importance: High

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Ginny Portner Remsen Building Art Unit 1645 Room E03, B02; Mail Box 3C18 (571) 272-0862

----Original Message-----**From:** Portner, Ginny

Sent: Friday, August 04, 2006 11:32 AM

To:Subject: 09/904994 nucleic and amino acid sequence search with specific gap values; claims attached

Importance: High

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Ginny Portner Remsen Building Art Unit 1645 Room E03, B02; Mail Box 3C18 (571) 272-0862

In the claims:

Claims 1 - 22 (Canceled)

23. (Currently amended) A ducloic acid molecule comprising a nucleotide sequence encoding two <u>urease X and urease Y</u> subunit polypeptides of a urease complex such as expressed by Helicobacter felis, said nucleotide sequence having at least 85% homology with SEQ ID NO: 1 or a part thereof encoding at least an immunogenic fragment of one of said subunits, said part having a length of at least 40 ZD nucleotides.

34. (Currently amended) An isolated Halicohacter felis urease X subunit polypeptide, said polypeptide comprising an umino acid sequence that is at least 85% homologous to SEQ ID NO: 2, or an immunogenic fragment of said polypeptide having a length of at least 40 70 amino acids, wherein said immunogenic fragment induces an immune response against an urease X subunit in urease XY.

Attorney Docket: I-2000.566 US

Response to Office Action of November 21, 2005

Amendments to the Claims:

min longth = 70

1. - 22. (cancelled)

- 23. (currently amended) [[A]] An isolated nucleic acid molecule comprising
- (i) a nucleotide sequence encoding urease X and urease Y subunit polypeptides of a urease complex expressed by *Helicobacter felis*, said nucleotide sequence having at least 85% homology with SEQ ID NO: 1 as determined over a global alignment wherein the mismatch value is 1, the open gap value is 3 and the extended gap value is 3; or

 (ii) a part thereof of (i) encoding at least an immunogenic fragment of one of said subunits, sai
- (ii) a part thereof of (i) encoding at least an immunogenic fragment of one of said subunits, said part having a length of at least 70 nucleotides.

24. - 25. (cancelled)

- 26. (original) The nucleic acid molecule of claim 23, which encodes one or both of the urease X subunit polypeptide and urease Y subunit polypeptide.
- 27. (cancelled)
- 28. (currently amended) The nucleic acid molecule of claim 23, wherein the nucleotide sequence has at least 94% homology with SEQ ID No: 1 as determined over a global alignment wherein the mismatch value is 1, the open gap value is 3 and the extended gap value is 3.
- 29. (cancelled)
- 30. (previously presented) An isolated and purified DNA fragment comprising a nucleotide sequence according to claim 23.

Attorney Docket: 1-2000.566 US

Response to Office Action of November 21, 2005

- 31. (original) A recombinant DNA molecule comprising a nucleotide sequence according to Claim 23 under the control of a functionally linked promoter.
- 32. (original) A live recombinant carrier comprising a recombinant DNA molecule of claim 31.
- 33. (original) A host cell comprising a nucleic acid molecule of claim 23, a DNA fragment of claim 30, a recombinant DNA molecule of claim 31 or a live recombinant carrier of claim 32.
- 34. (currently amended) An isolated *Helicobacter felis* urease X subunit polypeptide, said polypeptide comprising
- (a) an amino acid sequence that is at least 85% homologous to SEQ ID NO: 2 as determined over a global alignment wherein the mismatch value is 2, the open gap value is 4 and the extended gap value is 1; [[,]] or
- (b) an immunogenic fragment of (a) said polypeptide having a length of at least 70 amino acids, wherein said immunogenic fragment induces an immune response against [[an]] a urease X subunit in ureaseXY.
- 35. -36. (cancelled)
- 37. (currently amended) The polypeptide of claim 34, wherein said polypeptide comprises:
- (i) an amino acid sequence that is at least 90% homologous to SEQ ID NO: 2 as determined over a global alignment wherein the mismatch value is 2, the open gap value is 4 and the extended gap value is 1; [[,]] or
- (ii) an immunogenic fragment of said-polypeptide which (i) having a length of at least 70 amino acids;

wherein said immunogenic fragment induces an immune response against [[an]] a urease X subunit in ureaseXY.

Attorney Docket: I-2000.566 US

Response to Office Action of November 21, 2005

- 38. (currently amended) The polypeptide of claim [[37]] 34, wherein said polypeptide comprises:
- (i) an amino acid sequence that is at least 94% homologous to SEQ ID NO: 2 as determined over a global alignment wherein the mismatch value is 2, the open gap value is 4 and the extended gap value is 1; [[,]] or
- (ii) an immunogenic fragment of said polypeptide which (i) having a length of at least 70 amino acids;

wherein said immunogenic fragment induces an immune response against [[an]] a urease X subunit in ureaseXY.

- 39. (currently amended) The polypeptide of claim [[31]] 34, wherein said polypeptide comprises:
- (i) an amino acid sequence that is at least [[97%]] 99% homologous to SEQ ID NO: 2 as determined over a global alignment wherein the mismatch value is 2, the open gap value is 4 and the extended gap value is 1; [[,]] or
- (ii) an immunogenic fragment of said-polypeptide which (i) having a length of at least 70 amino acids;

wherein said immunogenic fragment induces an immune response against [[an]] a urease X subunit in ureaseXY.

- 40. (currently amended) An isolated *Helicobacter felis* urease Y subunit polypeptide, said polypeptide comprising
- (a) an amino acid sequence that is at least [[85%]] 86% homologous to SEQ ID NO: 3 as determined over a global alignment wherein the mismatch value is 2, the open gap value is 4 and the extended gap value is 1; [[,]] or
- (b) an immunogenic fragment of (a) said polypeptide having a length of at least 70 amino acids, wherein said immunogenic fragment induces an immune response against [[an]] a ureaseY subunit in ureaseXY.

Attorney Docket: 1-2000.566 US

Response to Office Action of November 21, 2005

41.- 43. (cancelled)

44. (currently amended) The polypeptide of claim 40, wherein said polypeptide comprises:

(i) an amino acid sequence that is at least [[94%]] 98% homologous to SEQ ID NO: 3 as determined over a global alignment wherein the mismatch value is 2, the open gap value is 4 and the extended gap value is 1; [[,]] or

(ii) an immunogenic fragment of said polypeptide, which (i) having a length of at least 70 amino acids;

wherein said immunogenic fragment induces an immune response against [[an]] a urease Y subunit in ureaseXY.

45. (cancelled)

46. (previously presented) An immunogenic composition comprising an immunogenically effective amount of a nucleic acid molecule of claim 23 and a pharmaceutically acceptable carrier.

47. (previously presented) The immunogenic composition of claim 46, further comprising an adjuvant.

- 48. (previously presented) The immunogenic composition of claim 46, further comprising an additional antigen derived from a virus or microorganism which is pathogenic to mammals.
- 49. (previously presented) The immunogenic composition of claim 48, wherein said virus or microorganism pathogenic to mammals is selected from the group consisting of Feline Infectious Peritonitis virus, Feline Immune deficiency virus, Canine Parvovirus, Feline Parvovirus, Distemper virus, Adenovirus, Calicivirus, Bordetella bronchiseptica, Borrelia burgdorferi,

Attorney Docket: I-2000.566 US

Response to Office Action of November 21, 2005

Leptospira interrogans, Chlamydia and Bartonella henseli.

50. (previously presented) An immunogenic composition for combating *Helicobater felis* infections, comprising antibodies against a polypeptide of claims 34 or 40.

51.- 56. (cancelled)

- 57. (previously presented) An immunogenic composition, comprising an immunogenically effective amount of a polypeptide according to Claim 34 and a pharmaceutically acceptable carrier.
- 58. (previously presented) An immunogenic composition, comprising an immunogenically effective amount of a polypeptide according to claim 40 and pharmaceutically acceptable carrier.
- 59. (new) The polypeptide of claim 40, wherein said polypeptide comprises:
- (i) an amino acid sequence that is at least 99% homologous to SEQ ID NO: 3 as determined over a global alignment wherein the mismatch value is 2, the open gap value is 4 and the extended gap value is 1; or
- (ii) an immunogenic fragment of (i) having a length of at least 70 amino acids; wherein said immunogenic fragment induces an immune response against a urease Y subunit in ureaseXY.

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A72509 Sequence 1 A73285 Sequence 1

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Helicobacter felis
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraces; Helicobacter.

1 (bases 1 to 2883)
Kusters,J.G. and Cattoli,G.
Helicobacter felis vaccine
Patent: JP 2002355054-A 1 10-DEC-2002;
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K69080 H.felis ure
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PN JP 2002355054-A/1
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PP 16-JUL-2001 JP 2001214711
PR 17-JUL-2000 EP 00202565.8
PI JOHANNES GERARDUS KUSTERS, GIOVANNI CATTOLI
PC
C12N15/09, AG1X38/00, AG1X39/106, AG1X39/118, AG1X39/12, AG1X39/175, PC
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C12R1:01),

PC C12N15/00,C12N5/00,A61K37/02

CC Helicobacter felis vaccine

FH Key Location/Qualifiers

FT CDS (886)

FT CDS (897)..(2603).
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JP 2002355054-A/1
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16-JUL-2001 JP 2001214711
17-JUL-2000 BP 00202565.8
JOHANNES GERARDUS KUSTERS,GIOVANNI CATTOLI
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GGMVVFSEMGDSVASVPTPQPVYYREMFGHIGKAKPDTSITFVSKVAYENGVKEKLGL
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Akzo Nobel N.V. (NL)
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                                                      RGGRAGATTTTCCARCACTTCAAGCACATATTGATCCTGTGTTGTGGGGTGGTAAATTRCR
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100.0%; Score 2880.6;
100.0%; Pred. No. 0;
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Helicobacter felis Helicobacter felis Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.

Kusters, J.G. and Cattoli, G. Helicobacter felis vaccine

REFERENCE AUTHORS TITLE

PAT 13-FEB-2002

linear

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Sequence 1 from Patent EP1176192. AX356683 AX356683.1 GI:18674020

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DD 1561 ACTGGGGCACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAATACGATG 1620	Qy 1621 TGCAAGTTTGTATCCACCGATACAGTCAATGAGGCAGGTTATGTAGATGACACCCTAA 1680 Db 1621 TGCAAGTTTGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATGACACCCTAA 1680	QY 1681 ATGCAATGAAGGGGGCGTCCATGCCTACCACATTGAGGGAGG	OY1741 CACCTGATGTTATCACCATGGCAGGGGAGGTCAATATTCTACCCTCCTCCTCCACCCCCA 1800 DD	OY 1801 CTATTCCCTATACATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGCCACC 1860 DD 1801 CTATTCCCTATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGCCACC 1860	OY 1861 ACCTAGACAACGCATCCGCGAGGATTTACAATTTTCTCAAAGCCGTATCGCCCCGGGCT 1920	1921 CTATGGGGGCTGAAGATGTGCTCCATGATATGGGTGTGATGGGATGACAAGCTCGGATT 	1981 CGCAAGCAATGGGGGGGGGGGGGGGTGATTCCTCGAACTTGGCAGACTGGGGGTAAGA 	2041	2101 AGGGCTACATCTCCAAATACACTATCAACCCGGCTTTGACCCACGGGGTGAGGGATTA 2101 AGGGCTACATCTCCAAATACACTATCAACCCGGGTTTGACCCACGGGGGGGG	2161	2221	Qy 2281 CTAACGCGTCTGTGCCCACTCCCCAACCGGTTTATTACCGCGAAATGTTTGGGCATCACG 2340 D 2281 CTAACGCGTCTGTGCCCCCCCCCCCCACCGCGTTTATTACCGCGAAATGTTTGGGCATCACG 2340	2341	Oy 2401 TGAAAGAAAAGCTGGGCTTAGAGCGCCAAGTTCTACCGGTCAAAAACTGCCGTAACATCA 2460	OY 2461 CCAAGAAAGACTTCAAGTTCAACGACAAAACGGCAAAAATCACGGTCGATCCGAAAACCT 2520	OY 2521 TCGAGGTCTTTGTAGATGGCAAACTCTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAG 2580 DD 2521 TCGAGGTCTTTGTAGATGGCAAACTCTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAG 2580	QY 2581 CCCAGGGGTACACTTTCTTCTAGGCACAATGCCCCCTTTGGGGGGCAGGTTATTTTAGGAA 2640 Db 2581 CCCAGGGCTACACTTTCTTCTAGGCACAATGCCCCCTTTGGGGGCAGGTTATTTTAGGAA 2640	QY 2641 TCTTCATCAAACGCACCTGCAATCGGTCTTGCGTGTGCGATCGTGTCGCTTTAAAACAAC 2700
481 ACTTGTAACTGGAATTGGCCCATCGAACCAGATGAGCACTTCAAAGCCGGGCGAAGTGAA 540	ATTIGGTIGGATAAAGACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACTTGAGGT 600 ATTIGGTIGCGATAAAGACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACTTGAGGT 600 ATTIGGTIGCGATAAAAAAAAAAAAAAAAAAAAAAAAAAA	TACTAATGAAGGGCCTAAATCCTTGCATGTGGGTAGCCATTTCCACTTCTTTGAAGCTAA 660 TACTAATGAAGGGCCTTAAATCCTTGCATGTGGGTAGCCATTTTCACTTCTTTGAAGCTAA 660 TACTAATGAAGGCCCTTAAATCCTTGCATGTGGGTAGCCATTTTCACTTTTTGAAGCTAA 660	TACTARISMAGGGCCTARATICCTIGCATGTGGGGAAACGCCTAGATTTCCTTTTGAAGGTAA 880 CAAGGCACTAAAATTCGATCGTGAAAAAGCCTATGGCAAAGGCTAGATATTCCCTCTGG 720 CAAGGCACTAAAATTCGATCGTGAAAAACCTATGGCAAACGCCTAGATATTCCCTCTGG 720	CAACACGCTATGGGGCAGGACAAACCGCAAAGTGCAGTTGATTCCTCTTGGGG 780	CAGTAAAAAAGTGATTGGCATGAACGGGCTTGTGAATAACATCGCGGATGAACGCCATAA 840	ACATAAAGGGCTTGACAAGGGAAATCTGAGGATTTATCAAGTAAGGAGACTCCATGA 900	096	TAGGAGATACCGATCTTTGGGCAGAAGTAGACATGACTATACCACCTATGGCGAAGAAC 1020 	1080	1140	AAGCCGACATTGGGATTAAAAACGGCAAAATCCATGGCATTGGCAAGGCAGGAACAAGG 1200 	ACATGCAAGATGCCGTCATATGGTCGTGGGTGTGGGCACAGAAGCACTAGCAG 1260	GGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACCCCACTTCCTTTCTCCAC 1320 GGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACCCCACTTCCTTTTCTCCAC 1320 GGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACACCCCACTTCCTTTCTCCAC 1320	AACAATTCCCTACGCTCTAGCCAATGGCGTTACAACCATGTTTGGAGGCGGCACAGGTC 1380	CTGTAGATGGCACGATGTATCACTCCGGGCAAATGGAACTTGCACCGCATGT 1440 CTGTAGATGGCACGAATGCGACTATCACTCCGGGCAAATGGAACTTGCACCGCATGT 1440 CTGTAGATGCCACGAATGCACTATCACTTATCACTTATCACTTGAATTGCAACTTGCAACTTTGTATTATTATTATTATTATTATTATTATTATTATTAT	TGCGCGCAGCAGAATTTTTTTTTTTTTTTTTTTTTTTTT	GCAAAAAACAACTIGTAGAACAAGTAGAAGGGGGGGGGGG	1501 GCAAAAAACAACTIGIAGAACAAGIAGAGGGGGGGGTTIGGTITIAAATIGGATGAAG 1560 1561 ACTGGGGCACAACACCAAGIGGGATCGATCACTIGGTGGGGGGAATGAATACGAIG 1620

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CCAAAGAGCAAGAAAAGTTCTTGTTATTATGCGGGGGGAGGTGGCTAGAAAGCGCAAAG 120
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                                                                          121 CAGAGGGTTAAAGCTCAACCAACCCGAAGCCATTGCCTACATTAGTGCCCATATTATGG
                                                                                                                        361 ACTITAAGGCGGGTGAAGTGAAATTTGGCTGTGATAAAGACATTGAACTCAACGCAGGTA
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                                                                                                                                                        181 ACGAGGCGCGTCGTGGCAAAAAACCGTTGCGGAACTTATGGAAGAGTGTATGCACTTTT
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Rusters, J.G. and Cattoli, G.
Helicobacter felis vaccine
Patent: JP 2002355054-A $ 10-DEC-2002;
                                                                                                                                                                        TTGTTTGGTGCTGGGCGCAAGGGTATTGAAACCCATCGCCTCAAAAAAGTAGAAGCCC 2880
                                                                                                                                                                                             TIGITIGGIGCIGGGCGCAAAGGGTAITGAAACCCATCGCCTCAAAAAAGTAGAAGCCAC 2880
 TCTTCATCAAACGCACCTGCAATCGGTCTTGCGTGTGCGATCGTGTCGCTTTAAAACAAC 2700
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C12N1/19,
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PN JP 200255054-A/5
PD 10-DEC-2002
PF 16-JUL-2001 JP 2001214711
PR 17-JUL-2000 EP 00202565.8
PI JOHANNES GERARDUS KUSTERS, GIOVANNI CATTOLI
PC CLINIS/09, A61K38/00, A61K39/116, A61K39/115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A61K39/23;
PC A61K59/235,A61K39/39,A61K39/395,A61P1/04,A61P31/04,C12N1/15
PC C12N1/19,
PC C12N1/21,C12N5/10,C12N9/80,C12Q1/68,G01N33/15,G01N33/50,G01N33/
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PC
601013/553,G010133/566,G010133/569//(C12N9/80,C12R1:01),(C12Q1/68,C12R1:01),

PC C12N15/00,C12N5/00,A61K37/02

CC Helicobacter felis vaccine
FF Key Location/Qualifiers
FT CDS (739). (728)

FT CDS (739). (2445).
                                                     1 AGGACTATAATCCCCATTGCCTTTAAAAATTTAACACAAGGAGTAATAGGTGAAACTCACAC
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Pred. No. 0;
0; Mismatches 140; Indels
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/organism="Helicobacter felis"
/mol_type="genomic DNA"
/db_xref="taxon:214"
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(739)..(2445).
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Helicobacter felis vaccine.
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Best Local Similarity 94.3%;
Matches 2312; Conservative
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Helicobacter felis
Helicobacter felis
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GAGGRISPDVTTMAGEVNILPSSTTPTINTAVBHLDMATCHHLDGVRIREDLQFS
OSRIRPGSIAAEDVLHDIGVIAMTSSDSQAMGRAGEVIPRTWQTADRUKKEFGKLPED
GADNDNRRIKRYISKYTINPALTHGVSEYIGSVEEGKIADLVVWNPAFFGVKRYIVE
GGWVVPSEMGDSNASVPTPQPVYYRENFGHGKAKFDTSITFVSKVAYENGYKEKLGL
ERKVLPPVKNCRNITKKOPKFNDKTAKIIVDPKTFEVFUDGKLCTSKPTSEVPLAQRYFF
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Helicobacter felis vaccine
Patent: EP 1176192-A 13 30-JAN-2002;
Akzo Nobel N.V. (NL)
Location/Qualifiers
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Helicobacter felis
Helicobacter felis
Helicobacter felis
Helicobacter felis
Helicobacteraceae; Helicobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.

El (bases 1 to 2407)
El (bases 2 to 2407)
El (bases 3 to 2407)
El (bases 4 to 2407)
El (bases 4 to 2407)
El Helicobacter felis vaccine

AKZO NOBEL NV
OS Helicobacter felis
PN JP 2002355054-A/4
PD 10-DEC-2002
PP 10-JUL-2000 EP 00202565.8
PP 10-JUL-2000 EP 0020265.8
PP 10-J
2281 CAAGACGCGCATATCACTGTCGATCCTAAAACCTTCGAGGTCTTTGTAGATGGCAAACT 2340
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Pp.
C12N13/566,G01N33/566,G01N33/569//(C12N9/80,C12R1:01),(C12Q1/68, 1)
C12N1:01),
PC C12N15/00,C12N5/00,A61K37/02
CC Helicobacter felis vaccine
FH Key
LocationQualifiers
FT CDS
(693). (632)
FT CDS
                                                CTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTAGGC
                                                                        2341 CTGCACCTCTAAACCCGCCTCTGAAGTGCCTCTAGCCCAACGCTACACTTTCTTCTAGGC
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/organism="Helicobacter felis"
//mol_type="genomic DNA"
/db_xref="taxon:214"
                                                                                                                                                                                                                                                                                                             DNA
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(693). (2399).
Location/Qualifiers
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Helicobacter felis vaccine.
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                                                                                                                                                                                                                                                     RESULT 7
BD185305
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VERSION
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AUTHORS
TITLE
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OSR I RPGSI AAEDVLHDI GYTAMYS SDSQAMGRAGEV I PRTWQTAHLDMLMTCHHLDXGF
SADNDNFRI KRYI SKYT INPALTHGVSEY I GSVEGKI ADLVWNPAFFEGVKKE FCKI. PE
GGWVVPS EMGDSNASYPTPQPVYYRENFGHGKAKPDTS I TFVSKVAY ENGYKEKI GIL
ERKVLPVKNCRNI TKKO FKFNNKTAHI I TVD PKTFEVFVDGKI. CTSKPASE VPLAQRYF
FF"
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DEHFRAGEVKFGCDFDIAAGKEVTELEYTNBGPKSILAVGSHFHFERANKALKFDRE
KAYGRKLDIPSGNTILRIGAGQTRKVQLIPLGSKKVIGMNGIVNNIADERHKHKALEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAD23262.1"
/db_xref="G1:18674031"
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GPVDGTNATTITPGKWNLHRMLRAAEEYSMNVGFLGKGNSSSKKQLVEQI EAGAI GFK
LHEDWGTTPSAI DHCLSVADEYDVQVCI HTDTVNEAGYVDDTLNAMNGRAI HAYHI EG
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codon start=1

/transl_table=11

protein_id="CAD23261.1"

db_xref="GI:18674030"
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/note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 2407
/organism="Helicobacter feli/mol_type="unassigned DNA"
/db_xref="taxon:214"
2. .682
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93.6%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                      Kusters,J.G. and Cattoli,G.
Helicobacter felis vaccine
Patent: EP 1176192-A 10 30-JAN-2002;
Akzo Nobel N.V. (NL)
                                                                                                                                                AX356692 2407 bp
Sequence 10 from Patent BP1176192.
AX356692
                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Epsilo
Helicobacteraceae, Helicobacter
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/transl_table=11
                                                                                                                                                                                                         AX356692.1 GI:18674029
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Helicobacter felis
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243 TTGGGCGTAGAAGCCACTTTCCCCGATGGCACCAACTCGTAACCGTGAATTGGCCCATT 302
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                                                                                                                      GAACCTGATGAACACTTTAAAGCCGGTGAAGTGAAATTTGGCTGTGATAAAGACATTGAG
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Helicobacter felis
Kusters, J.G. and Cattoli, G.
Helicobacter felis vaccine
AL Patent: JP 2002355054-A 3 10-DEC-2002;
AKZO NOBEL NV
OS Helicobacter felis
PP 10-DEC-2002
PP 116-JUL-2001 JP 2001214711
PP 116-JUL-2001 JP 2001214711
PP 11-JUL-2000 EP 00202555.8
PI JOHANNES GERARDUS KUSTERS, GIOVANNI CATTOLI
PC CI2NIS, OO, AGIK39/106, AGIK39/118, AGIK39/175, PC
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PC A61K39/235,A61K39/39,A61K39/395,A61P1/04,A61P31/04,C12N1/15,
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Pred. No. 0;
0; Mismatches 145; Indels
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    2183
/organism="Helicobacter felis"

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(694). (2181).
Location/Qualifiers
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/db_xref="taxon:214"
                                                                                                                                                                                                                                                        2183 bp
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Best Local Similarity 93.3
Matches 2035, Conservative
                                                         2606 ACAATG 2611
                                                                                                                2402 NCAATG 2407
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TITLE
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/translation="MKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIM DEARRGKKTVAELMEECMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEP DEHFKAGEVKFGCDKDIELNVGKEVTELEVTNEGFKSLHVGSHFHFFETNKALKFDRE KAYGKRLDIPSGNTLRIGAGQTRKVQLIPLGCSKKVIGMNGLVNNIADERHKHKALDK

AKSHGFIK"

683
 note="unnamed protein product"

codon_start=1 /transl_table=11 /protein_id="CAD23259.1" /db_xref="GI:18674027"

/organism="Helicobacter fe /mol_type="unassigned DNA" /db_xref="taxon:214"

P 1176192-A 7 30-JAN-2002; il N.V. (NL) Location/Qualifiers

us-09-904-994b-1.rge

1323 AGAAGCGGGCGATTGGCTTTAAATTGC/ 1586 ÇGATÇAÇTGÇTTGAGÇGTGGÇAGATGAATA	AGAAGCGGGCGCGATTGCCTTTAAATTGCATGAAGACTGGGGCACAACACCCAAGTGCGAT 1382 CGATCACTGCTTGAGCGTGGCAGATGAATACGATGTGCAAGTTTGTATCCACACGGATAC 1645	JOURNAL	L Patent: E Akzo Nobe
1383 CGATCACTGCTTGAGCGTGGCAGATGAATR	144	sourc	ırce
1646 AGTCAATGAGGCAGGTTATGTAGATGACAC 	agtcaatgaggcaggttatgtagatgacaccctaaatgcaatgaacgggggggcgcatcca 1705 	CDS	
1706 TGCCTACCACATTGAGGAAGCGGGTGGAGC	TGCCTACCACATTGAGGGAGGGGGGGGGAGGACTCACCTGATGTTATCACCATGGCAGG 1765 		
1766 CGAGCTCAATATTCTACCCTCCTCCACCACCACCACCACCACCA	CGAGCTCAATATICTACCCTCCTCCACCACCCCCCATTATTCCCTATACCATTAATACGGT 1825 		
1826 TGCAGAACACTTAGACATGCTCATGACATC	TGCAGAACACTTAGACATGCTCATGACATGCCACCACTAGACAAACGCATCCGCGAGGA 1885 	CDS	
1886 TITACAATITICTCAAAGCGTATCCGCCC	TITACAATITICTCAAAGCCGTATCCGCCCCGGCTCTATCGCGGCTGAAGATGTGCTCCA 1945 		
1946 TGATATGGGTGTGATCGCGATGACAAGCTC	TGATATGGGTGTGATCGCGATGACAAGGTTCGGATTCGCAAGCAA		
2006 AGTGATTCCTCGAACTTGGCAGACTGCGGA 	agtgattcctcgaacttggcagactgcggataagaataaaaagaatttggtaagcttcc 2065 		
2066 TGAAGATGGCAAAGATAACGATAATTTCCG	TGAAGATGGCAAAGATAACGATTTCCGCATTAAGCGCTACATCTCCCAAATACACTAT 2125 	ORIGIN Query Best I	
2126 CAACCCCGCTTTGACCCACGGGGTGAGGGATATATCGGCTCTGTGGAAGAGGGCAAGAT 	CAACCCGGTTTGACCCACGGGGTGAGGAGTATATCGGCTCTGTGGAAGAGGGCAAGAT 2185 	Macche	Macches 2035; Cons 206 GTGAAAC
2186 CGCCGACTTGGTGGTGGAATCCTGCCTT	CGCCGACTTGGTGGTGTGGATCCTGCCTTTTTTGGCGTAAAACCCAAAATCGTGATCAA 2245 	g &	
2246 AGGCGGTATGGTGGTCTTCTCTGAAATGGG 	AGGCGGTATGGTGTTCTTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCACTCCCCA 2305	g &	63 AGAAAGC 326 GCCCATA
2306 ACCGGTTTATTACCGCGAAATGTTTGGGCAATCGGCAAAGTTTGACACCAGCAT 	ACCGGTTTATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTTGACGCCACGT 2365 	do yo	123 GCCCATA 386 TGCATGC
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2163 CACTTTTCGTGTCTCAAGCG 2182		충 옵 	
AX356689 AX356689 2183 bp	DNA linear PAT 13-FEB-2002	& 8	506 GAACCAG 303 GAACCTG
DEFINITION Sequence 7 from Patent EP1176192. ACCESSION AX356689.1 GT:18674026 AX356689.1 GT:18674026		ò.	
		qa	363 CTCAACG
ORGANISM Helicobacter felis Bacteria: Proteobacteria: Ebsilo	Helicobacter felis Bacteria: Proteobacteria: Epsilonproteobacteria: Campylobacterales:	ð	626 CATGTGG

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Helicobacter felis Helicobacter felis Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

Kusters, J.G. and Cattoli, G. Helicobacter felis vaccine

REFERENCE AUTHORS TITLE

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gene cluster
DNA Seq. 13 (6), 321-331 (2002)
12652903
Zhu, J. and Chang, Y.F.
Direct Submission
Submitted (21-DEC-2000) Population Medicine and Diagnostic Science,
College of Veterinary Medicine, Cornell University, Tower Road,
Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF330621 BCT 13-MAY-2003 Helicobacter bizzozeronii tRNA ribosyltransferase gene, partial cds; GidB, complete cds; urease gene cluster, complete sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter bizzozeronii
Helicobacter bizzozeronii
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.

(bases 1 to 8406)
Zhu,J., Tengy,C.H., Chang,C.F., Chang,C.D., Simpson,K.W., Wei,C.,
Chonough,P., McDonough,S. and Chang,Y.F.
Cloning and characterization of a Helicobacter bizzozeronii urease
               CGCCGACTTGGTGGTGTGGAATCCTGCCTTTTTTTGGCGTGAAACCTAAGATTGTGATTAA
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                                                                                                                                                    TGAAGATGGCAAAGATAACGATAAATTTCCGCATTAAGCGCTACATCTCCAAATACACTAT
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                                                                                                      rrracaartrrcrcaaagccgrarccgccccggarcrarrgccgcrcaaggargrcca
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                                                                                                                                    AGTGATTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAAGAATTTGGTAAGCTTCC
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                                                                          TTTACAATTTTCTCAAAGCCGTATCCGCCCCGGCTCTATCGCGGCTGAAGATGTGCTCCA
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/db_xref="taxon:56877"
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                                             CAAACCCGTAAAGTGCAGTTAATCCCTCTTGGCGGTAGTAAAAAAGTGATTGGCATGAAC
                                                                                                         GGGCTTGTGAATAATATTGCGGACGAACGCCATAAACACACAAAGCCCTTGGAATAATAATAATAATAAACACGAAAAA
                                                                                                                                                                     CCGTGAGGGTATGGGTCAGAGCAATAGCCCAGATGAAAACACCTTAGATTTAGTGATCAC
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                                                                                         Candidatus Helicobacter Helimannii
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.

1 (bases 1 to 2664)
Solnick,J.V., O'Rourke,J., Lee,A. and Tompkins,L.S.
Molecular analysis of urease genes from a newly identified
uncultured species of Helicobacter
Infect. Immun. 62 (5), 1631-1638 (1994)
8168924
On May 3, 1995 this sequence version replaced gi:529422.
Original source text: Helicobacter heilmannii (individual_isolate
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    organism="Candidatus Helicobacter"

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Pred. No. 0;
1; Mismatches
                                                                   urease.
Candidatus Helicobacter heilmannii
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	RESULT 13 AE001439 00/C WPCOMMENT Sequence split into 17 fragments LOCUS AE001439 Accession AE001439 Fragment Name Begin End AE001439 01 110000 AE001439 01 100001 210000 AE001439 04 400001 310000 AE001439 04 400001 510000 AE001439 04 600001 710000 AE001439 05 600001 710000 AE001439 07 700001 810000 AE001439 07 700001 810000 AE001439 07 700001 910000 AE001439 07 700001 910000	100001 1100001 1200001 1300001 1400001 1500001 439 AB001440-ARD 439.1 GI:120572		DUDRINAL Natures 397 (6715), 176-180 (1999) PUDRING 992682 REPERENCE 2 (bases 1 to 164381) RIGHORN King, B. L., Ahm, R. A. and Trust, T.J. AUTHORS Licet Submission JOURNAL Submitted (12-JAN-1999) Astra Research Center Boston, 128 Sidn Street, Cambridge, MA 07139, USA COMMENT On or before Jan 19, 2006 this sequence version replaced gi:4154501, gi:4154511, gi:4154633, gi:4154549, gi:4154666, gi:4155679, gi:4154626, gi:4154639, gi:4154651, gi:4154666, gi:4154679, gi:4154699, gi:4154709, gi:4154713, gi:4154789, gi:4154869, gi:4154880, gi:4154886, gi:4154886, gi:4154889, gi:4154880, gi:4154880, gi:4154910, gi:4154910, gi:4154899, gi:4155499, gi:4155005, gi:4155004, gi:4155004, gi:41550974, gi:4155006, gi:4155008, gi:4155100, gi:4155102,
1292 CGATTCACACCCCACTTCCTTTCTCCACAACTACTCCCTACCGCCTAGGCGATGGCGT 1351		CATATTCTACCTCCTCCACCACCACATTCCTATACATTATACGTTGCAGA TAACATCTTCTCTCTCTCTCTCTTTCCTATACGTTGCAGA TAACATCTTCTCTCTCTCTCTCTCTTTCCTTTACCATAACACAGAGCCGA ACACTTAGACATGCTCTTCTCCTCTTTCCCTTTCCCAAAACACAGAGCCCAAACACACAC	1952 GGGTGTGATCGCAATGCTCGCAAGCAATGGGGGCGTGCAGGCAAGTGAT 2011	2132 CGCTTTGACCCACGGCGTGAGCGAGTATATCGGCTCTGTGGAAGAGGCAAGATCGCCGA 2191 2165 TGCCATCACACACACGCATTTCTGAATATCTGGCTTGTAGAAGTGGGTAAATACGCTGA 2224 2192 CTTGGTGGTGGTGAATCTGCCTTTTTTGGCGTAAAACCCAAATCGTGATCAAAGGCGG 2251 2225 CTTGGTGGTTTTTGGCGTTTTTTGGCGTAAAACCCAACTGATCAAAGGCGG 2284 2225 TATGGTGCTTTTTTGGCGTTCTTTGGCATTAAAACCCAACTGATCAAAGGCGG 2284 2228 TATGATTGCGCTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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AGATGGCAAACTCTGCAC 2551
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                                        CAAGTTCAACGACAAAAC 2491
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|raagtTCAACGATGTCAC 2524
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, deJonge, B.L.,
kelsen, M., Mills, D.M.,
Jiang, Q., Taylor, D.E.,
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|CCTATTCTAG 2636
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DSSPPPILPRAAAVGI DGIEPAETHIDPKNALSDGANMLKPDBLEHLVTDMLKI QNLF
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AIKEALGKGFILTLPGIRLDKNDKEDGRVANAKEAKQNLSDFIVVGRPIYQAKEPRE
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                        H. pylori 26695 gene HP0003
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complement(1766. .2431)
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3235. .4065
                        note="similar to
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/gene="panC'
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complement(51. .467)
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000; Gaps	TATTAC	TTTAAA	AAAACA	TTGTTA	ATGCTC	CAACCO		AAGACT	999333 -	GATĠĞT	AAACTT	PAACTO	AAATTTG		GTTAAA	AACAAG		GGCAAC	GGGACA	GGCAGT	GGCAAC	AAACAT		AACTAT	AATACC	TCTATG	GAAGTA	GAAGTA	ATCCGT	ACTAAC
gth 11000 s 39;	TAATAT	PATTGC	III Saaggaa	AAAGTTC	PAGTTG	SCTCAAC		GGTAAA	AGTAATG	rGTGATG	rggtace	rgggacc	GAAGTO	CHECKLING	CGTGAAP	rgaagci	 GAAGTG	rcccrc	rgcgago	rcrrgg	CATTGG	ACGCCAT		CGATGAC	ATATGE	ATATGT	TTGGGC	gatccc'	TAAAAC	AGTCAT
; Len Indel	TATATA CTTCTG	TAATCC	 TGTCTT(GCAAGA	GTTAGA:	CTTAAAC		GAGAGC	AGATGA	GGATGA	TCCTGA	TCCTGA	AGCGGG		CGTTAG	CTTCTT	TTTCTT	AGATAT	AGACAT	GATTCC	GATTGA	GGATGA		TAAAAG	ACAAGA	AAAAGA	CGATCT	AGALTL		AGATTT
DB 15 e-313; 853;	ATTATCA ATAAACG	AGGACTA	 GCGTTA	CCAAAGA	CAAAAGA	CAGAGGG		AAGAAGC	rgaaaaa 	FAAAACC	CCACCTT	CGATGTT	ACTTCAA ATTCCT	1991 TAG	H	ATTTCCA	ACTTCCA	AACGCCT	AACGCTT	rgcagtt	ragaatt	ACATOGO		ATGGTGC	TGAAAAA	TTAGCAG	GAGATAC	GCGATAC	AATTTGG	ACACCCI
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38;	ATTTTT TTTAAA	AATAAA	CAATTA	TAATAG	AATGAG	GTGGCT	TOOL IN	ATTAGE	SGAAGAG	CAAGAA	CCCGAT	CATGAA	SCCCATO		ATCACT	ATCCTTG	ACCGGTT	CGTGAA	AGAGAA	SGCAGGA	SCCTGGC	CATGAAC	GCGAAA	 AGCTAAA	GAGACT	GAGTAA	AGGCGAT	AGGCGAT	CACCTAT	BAGCAAT
36 ty 65 ervativ	ATTATTA 	AAAAGTT	 ATTGCT?	CAAGGAC	ATAGGAC	33333333333333333333333333333333333333		AGCTTTC	GCTTATC	ATTGATO	TATGGT	CATGATO	GAATTGC	CAIAC	TGAAGAC	GCCTAA	CGACAG	ATTCGA1	CTTTGAC	CATTGG	GTTTGAC	GATTGG	TGACAAC	ACACAG	AAGTAAC	AATTAA	CACCAA	TACCAC	CTATAC	GGGTCAC
36. Similarity 65. 1; Conservative	AATRCT	ATATTA	CAAAAG	TTAACA	TTAAGA	ATTATGO		AGCGGT.	TGCCCA	GĠĊTGĂ	GGGTAA	rggcaag	PACTGT	THOUGH.	 - aaaaaa	TGAAGG	ACGTGGG	CACTAAA	SCCTAGA	SGCTACG	GGTAAG	AAAAAGT	VAGCGCT	 rtgcttt	ATC	raaaaac	ACGGACC	TGGCCC	AACATGA	AGGGTAT
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Tomb, J.-F., White, O., Kerlavage, A.R., Clayton, R.A., Sutton, G.G., Pleischmann, R.D., Ketchum, K.A., Klenk, H.P., Gill, S., Kirkness, B.F., Bougherty, B.A., Melson, K., Quackenbush, J., Zhou, L., Kirkness, B.F., Glodek, A., McKenney, K., Pictagerald, L.M., Lee, N., Adams, M.D., Hickey, E.K., Berg, D.B., Gocayne, J.D., Utterback, T.R., Peterson, J.D., Kelley, J.M., Cotton, M.D., Weidman, J.M., Fujii, C., Bowman, C., Watthey, L., Wallin, B., Hayes, W.S., Borodovsky, M., Direct Submission
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Submitted (17-WAR-1999) The Institute for Genomic Research,
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gi:2314060,
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complement (635. .1105)
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/protein_id="AAD07074.1"
/db_xref="GI:2313078"
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Nature 388 (6642), 539-547 (1997)
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/locus_tag="HP_0001"
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/transl_table=11
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Bacteria, Proteobacteria; Epsilonproteobacteria; Campylobacterales; Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.

I (bases 1 to 1667867)
S Tomb,J.-F., White,O., Kerlavage,A.R., Clayton,R.A., Sutton,G.G., Fleischmann,R.D., Ketchum,K.A., Klenk,H.P., Gill,S., Dougherty,B.A., Nason, K., Quackenbush,J., Zhou,L., Kirkness, B.F., Peterson,S., Loftus,B., Richardson,D., Dodson,R., Khalak,H.G., Glodek,A., McKenney,K., Fitzegerald,L.M., Lee,N., Adams,M.D., Hickey,B.K., Berg,D.B., Gocayne,J.D., Utterback,T.R., Peterson,J.D., Kalley,J.M., Karp,P.D., Smith,H.O., Fraser,C.M. and Vonter,J.C.

The complete genome sequence of the gastric pathogen Helicobacter
73503 CAGCGATCGCTCATGGGATTAGCGAGTATGTAGGTTCTGTAGAAGTGGGCAAAGTGGCTG 73444
                                                                                                                                                                                                                 73383 GATTCATTGCGTTAAGCCAAATGGGCGATGCGAACGCTTCTATCCCTACCCCACAACCGG 73324
                                                                                                                                                                                                                                                                                                                                                                                                                                   73263 TTGTGTCTCAAGCGGCTTATGACAAAGGCATTAAAGAAGAATTAGGGCTTGAAAGACAAG 73204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73203 TGTTGCCGGTTAAAAATTGCAGAAACATCACTAAAAAAGACATGCAATTCAATGACACTA 73144
                                                                                                          73384
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                                                                                   73143 CCGCTCACATTGAAGTCAATCCTGAAACTTACCATGTGTTCGTGGATGGCAAAGAAGTCA
                                                     ACTIGGIGGIGIGGAATCCTGCCTTTTTTGGCGTAAAACCCAAAATCGTGATCAAAGGCG
                                                                                                                                                               GTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCACTCCCCAACCGG
                                                                                                                                                                                                                                                                       TTTATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTTGACACCAGCATCACTT
                                                                                                                                                                                                                                                                                                                                                                              CGGCAAAAATCACCGTCGAAAACCTTCGAGGTCTTTGTAGATGGCAAACTCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73083 CTTCTAAACCAGCTAATAAAGTGAGCTTGGCTCAACTCTTTAGCATTTTCTAGG 73030
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26695, complete genome.
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AE000511 AE000523-AE000656
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complement (1115. 11945)
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ETALKNGVMLCERGSSFGYGNIVVDMRSLKTMREPAPVIFDATHSYQMPGGANGKSSG
DSSFAPILARAAAAVGIDGLFAETHVDPKNALSDGANMLKFDBELEQLVTDMLKIQNLF
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/tb_xref
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GACGSVHLIHDETTKAKTPYIANWIQPLEPVKEELKNHPQPSNHFAKRSWLTERLNAR
LQLNNLLSYDFIQEKASKNELKIFGWHYIIETGRIYNYNFESHFFEPIGETIKQRKSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
/product="3-deoxy-d-manno-octulosonic acid 8-phosphate
synthetase (kdsA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GP:1359596 percent identity: 53.41; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="HP_0006"
hote="similar to PID:1146241 SP:P52998 GB:AL009126
percent identity: 44.24; identified by sequence
similarity; putative"
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/locus tag="HP 0005"
/note="similar to GB:M59757 SP:P25971 PID:143393
GB:AL009126 percent identity: 38.97; identified leaquence similarity; putative"
/codon.start=1
/transl_table=11
      52.45;
                                                                                                                             beta chain (ribE)
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/protein_id="AAD07079.1"
/db_xref="GI:2313083"
PID:1221434 PID:1205541 percent identity: 52 identified by sequence similarity; putative"
                                                                                                                       /product="riboflavin synthase
/protein_id="AAD07075.1"
/db_xref="GI:2313079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAD07076.1"
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2719. .3402
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complement(1932..25
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/transl_table=:
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77499 GCTTAGACTTTGACAGAGAAAAACTTTCGGTAAACGCTTAGACATTGCGAGCGGACAG 77440
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/translation="MRVLETIVALREYRKSLEESVGFVPTMGALHKGHQSLIERSLKE
NENTIVSVGFVWPTQFGANEDRAYPFELEKDLELCERLGYWAPVFDKTGEMYPYSEAEQ
RLKLYAPKELSSSLEGAMRKGHFDGVVQIVLEMFHLWNPTRAYFGKKDAQQLLIIEHL
VKDLLLDIEIAPPCEIYGDDDNLALSSRNVYLMATQRKQALAIPKALEKIQQAIDKGEK
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                                                                                                                     ACEKLKKLGLE1LETLEVDYLECCNHKLEPLT11EPTNTL1LVAARVGKTRLLDNLWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77736 TGGCAAGCATGATCCATGAAGTGGGTATTGAAGCGATGTTTCCTGATGGGACAAAACTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 TIGCCCAGCTTATGGAAGAGTGCATGCACTTTTTGAAAAAAGATGAAGTAATGCCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGTAATATGGTTCCCGATCTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1029.2; DB 1:
Pred. No. 1.6e-309;
.; Mismatches 849;
                                                                                                                                                                                                                                                          complement (4250. .4322)
/locus tag="HP t01"
/product="tRNA-Glu"
/note="codon recognized: GAA"
complement (4388. .4461)
                                                                                                                                                                              .4322)
                                                                                                                                                                                                       /locus tag="HP t01"
/note="tRNA-Glu-1"
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75879 GGTTCATTGCGTTGAGTCAAATGGGTGACGGAACGCTTCTATCCTACCCTACCCAAACCAG 75820
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                                    TTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAGAATTTGGTAAGCTTCCTGAAG
                                                                                                                                                             75999 CAGCGATCGCTCATGGGATTAGCGAGTATGTAGGTTCTGTAGAAGTGGGCAAAGTGGCTG
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                                                                                                        CCGCTTTGACCCCACGGCGTGAGGAGTATATCGGCTCTGTGGAAGAGGGGCAAGATCGCCG
                                                                                                                                                                                                                                                                                                                                    GTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCCACTCCCCAACCGG
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                                                                                                                                           2071 ATGGCAAAGATAACGATAATTTCCGCATTAAGCGCTACATCTCCAAATACACTATCAACC
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Helicobacter pylori
Helicobacter pylori
Bacteria, Proteobacteria, Epsilonproteobacteria, Cam
Helicobacteraceae, Helicobacter.
I (bases 1 to 5100)
I Labigne, A., Cussac, V. and Courcoux, P.
Shuttle cloning and nucleotide sequences of Helicobagenes responsible for urease activity
J. Bacteriol. 173 (6), 1920-1931 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source text: H.pylori DNA
Location/Qualifiers .
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TITLE
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                                                       77259 TAAAAACAATTAAGGAGTAAGAAATGAAAAGATTAGCAGAAAAGAATATGTTTCTATGT
                           T---ATCAAGTAAGGAGACTCCCATGAAA---ATGAAAAACAAGAATATGTAAATACCT
                                                                                          ACGGACCCACCAAAGGCGATAAAGTGCGCTTAGGAGATACCGATCTTTGGGCAGAAGTAG
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                                       ACTACGCTGGAGAATTGGCTAAAAACGCAAAGAAAAAAGGCATTAAGCTTAACTATGTAG
                                                                                                                   AAGCAGTAGCTTTGATTAGTGCCCATATTATGGAAGAAGAGCGAGAGCTGGTAAAAAGACTG
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  ATTATGCGGGCGAAGTGGCTAGAAAGCGCAAAGCAGAGGGGCTTAAAGCTCAACCAGC
                                                                            366 TTGCCCAGCTTATGGAAGAGTGCATGCACTTTTTGAAAAAAGATGAAGTAATGCCCGGGG
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gene="urea"
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fene="urea"
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/ Gene="urea"
/ note="putative"
/ codon start=1
/ transl_table=11
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TFGKRLDIASGTANRFFEPGEEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRA
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                                                                        /translation="MKTFGTDGVRGKAGVKLJPMFVMRLGJAAGLYFKKHSQTNKILI
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                                                                                                                                                       GALHPNQLSQEVKKYRADLGFAFDGDADRLVVVDNLGNI VHGDKLLGVLGVYQKSKNA
LSSQAI VATRMSNLALKERTEKAFADLEBKRYGSEGRENRKARNGSGEGSGHI IF
SDYAKTGDGLVCALVOSALVLESKTUNSVELNPFELYPONLVNLAVOKKPPLESLKGY
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                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MLKTTKKSLLVPIGVPFLIFGVDQAIKYAILEGFRYESLVIDIV
LVFNKGVAFSLLSFLEGGLKYLQILLILGLFIFLMRQRELFKNHAIEFGMVFGAGVSN
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GAGGGHADDIIKVAGEHNILDASTNPTIPFTVNTRAEHMUNTCHHIDKSIKEDVQF
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EKGDNDNFRIKRYLSKYTINPAIAHGISBYVGSVEVGKVADLVUMSPAFFGVKPMII
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DMQDGVKNNLSVGPATEALAGEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGG
TGPADGTNATTITPGRRNLKMMLRAAEEYSMNLGFLAKGNASNDASLADQIEAGAIGF
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LERQYL PVKNCRN I TKKDMQFNDTTAH I EVNPETYHVFVDGKEVTSKPANKVSLAQL P
                                                                                                                                        AHLKHSFPKHLNLQSLRIVLDTANGAAYKVAPVVFSELGADVLVINDEPNGCNINEQC
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Pred. No. 3e-308;
1; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAA25019.1"
/db_xref="GI:149009"
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/db_xref="GI:149011"
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/codon_start=1
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/gene="ureD"
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/gene="ureD"
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Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of vaccines.
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P-PSDB; ADJ58238, ADJ58239.
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Adj58240 UreaseXY
Adj58240 UreaseXY
Adj58243 UreaseXY
Adj7847 H. bizzoz
Aa44351 H. bizzoz
Aa443560 H. felis
Aa475319 Urease ur
Aeb55130 Salmonell
Aeb55130 Salmonell
Aba00816 H. felis
Adj7850 H. bizzoz
Aba00816 H. felis
Aa414330 H. pylori
Aca34557 Prokaryot
Adu5558 DNA encod
                                                                     (without alignments)
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries

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Gapop 3.0 , Gapext 3.0
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Continuation (4 of
Acf68224 Photorhab
Ada30499 DNA encod
                                                     Continuation (6 of
Aca45232 Prokaryot
Aca45080 Prokaryot
Adf01572 Bacterial
Aca46520 Prokaryot
Adf05424 Haemophil
Adt05444 Haemophil
                                                                                                                                 Aav19002 Klebsiell
Aaz92097 Klebsiell
Ach96250 Klebsiell
Aca35953 Prokaryot
          Aal60579 Helicobac
Aaq04329 Probe for
Aba00817 H. pylori
Aav62460 Helicobac
                                                                                                                                                                            Aca34156 Prokaryot
Aca25712 Prokaryot
Aca23949 Prokaryot
Aca20910 Prokaryot
Aca20910 Prokaryot
Aca26184 Prokaryot
Aca44198 Prokaryot
Adu05359 DNA encod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenic fragment; antibacterial; Vaccine; Helicobacter felis; ds.
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897. _2603
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ACF65384_3
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ADT05644
AAV19002
AAZ92097
ACC96250
ACC35953
ACC334156
ACCA25712
ACCA53973
         AAL60579
AAQ04329
ABA00817
AAV62460
AAT42063
ACA45232
ACA45080
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ACA46520
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ACA20910
ACA26184
ACA44198
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The present invention relates to a novel Helicobacter felia urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis in Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an urease subunit polypeptide complex encoding sequence of the invention.
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                          100.0%; Score 2880.6; DB 7; Length 2883; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.
Matches 2883; Conservative
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                                                immunogenic fragment; antibacterial; Vaccine; Helicobacter felis;
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UreaseXY subunit encoding sequence #4
                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention relates to a novel Helicobacter felis urease X and
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                                     CGATCACTGCTTGAGCGTGGCAGATGAATACGATGTGCAAGTTTGTATCCACACCGATAC 1645
                                                     CGAGCTCAATATTCTACCCTCCTCCACCACCCCCATATTCCCTATACCATTAATACGGT 1825
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            AGAAGCGGGCGCGATTGGCTTTAAATTGCATGAAGACTGGGGCACAACACCAAGTGCGAT 1380
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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis. Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an
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93.6%; Pred. No. 0;
cive 0; Mismatches
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                                                                                                                                                                               UreaseXY subunit encoding sequence #3
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ADJ58246 standard; DNA; 2407
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P-PSDB; ADJ58247, ADJ58248.
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	TGCCTACCACATTGAGGGAGGGGGGGGGACACTCACCTGATGTTATCACCATGGCAGG	1825 TGCAGAACACTTAGACATGCTCATGACCACCTAGACCACCCCCCCC			2186 CGCCGACTTGGTGGTGTGGAATCCTGCCTTTTTTGGCGTAAAACCCAAAATGGTGATGAA 2245	2306 ACCGGTTTATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTTGACACCAGGAT 2365	2426 CCAAGTICTACCGGTCAAAAACTGCCGTAACATCACCAAGAAAGACTTCAAGGTTCAACGA 2485
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Best Local Similarity 93.3%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 145; Indels
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                                                                                                                                                      subunit encoding sequence #2
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                                                                                         ADJ58243 standard; DNA; 2183
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                                                GCCCATATTATGGACGAGGCGCCGTGGCAAAAAACCGTTGCTGAACTTATGGAAGAA
                                                                                                   183 TGTATGCACTTTTTGAAAAAAAGATGAGTGATGCCCGGTGTGGGGAATATGGTCCCTGAT
                                                                                                                                                                                                         CTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCCCATC
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, urease gene cluster, urease structural gene; accessory gene, ureABIEFGH; Helicobacter bizzozeronii infection;

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Chang Y, Simpson KW,

SIMPSON K W. ZHU J.

ZHUJ/) (SIMP/)

(CHAN/) CHANG Y

16-AUG-2002; 2002US-0404337P 12-AUG-2003; 2003US-00639273

H. bizzozeronii urease gene cluster, ureABIEFGH

(first entry)

07-OCT-2004

Urease; urease gene cluster;

Helicobacter bizzozeronii antibacterial; gene; ds.

US2004142343-A1

22-JUL-2004

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                                                                                                AGAAGCGGGCGCATTGGTTTTAAATTGCATGAAGACTGGGGCCACAACACCAAGTGCGAT
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                                           AGGCGGTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCACTCCCCA
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CACTITIGITICCAAAGICG 2385
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Helicobacter bizzozeronii an ability to produce urease, where the nucleic acid molecule is a urease gene cluster comprising at least one urease accessory gene. The nucleic acid molecule is chosen from urea, ureB, ureB, ureG, ureH and ureI. The invention also relates to an isolated protein encoded by the nucleic acid, a vaccine for preventing onset of disease in mammals infected by H. bizzozeronii comprising a nucleic acid and a carrier, and an isolated cantibody or its binding portion raised against the nucleic acid. The nucleic acids, proteins and antibodies are useful for vaccinating mammals antibody or its binding portion raised against the nucleic acid. The involves administering the sequences. The sequences are useful for detecting H. bizzozeronii in a sample of tissue or body fluids which involves providing a nucleic acid as an antigen, providing an antibody, or providing an uncleoide sequence as a probe in a nucleic acid or providing an uncleoide sequence as a probe in a nucleic acid or providing an antibody, and detecting any reaction which indicates that H. bizzozeronii is present in the sample. This sequence represents the H. bizzozeronii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule having urease gene cluster, and conferring on Helicobacter bizzozeronii ability to produce urease, useful as vaccine for preventing disease in mammals infected by H.bizzozeronii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2379 IGCATTATGCGGGCGAATTGGCTAAAAAACGCAAAGGCAAATGGCGTTAAGCTAAATTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 CCGTTGCCCAGCTTATGGAAGAGTGCATGCACTTTTTGAAAAAAGATGAAGTAATGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 AAATTTAACACAAGGAGTAATAGGTGAAACTCACACCCAAAGAGAGAAAAAGTTCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
39.4%; Score 1134.4; DB 12; Length 8407;
Best Local Similarity 68.5%; Pred. No. 3.9e-227;
Matches 1681; Conservative 0; Mismatches 741; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8407 BP; 2264 A; 1937 C; 1969 G; 2237 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 1; 40pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates
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GENBANK; AF330621.
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ADQ37847 standard; DNA; 8407

RESULT 6 ADQ37847

ADQ37847

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'note= "T7 promoter provides transcription initiation for
                                                                                                                                                                                                                                                   note= "Lac operator provides inducible expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine for inducing mucosal response to Helicobacter - contg. multimeric urease complex and pref. an antibiotic, anti-secretory agent or bismuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA clone (AAT44351), derived from pORV214, includes the ureA and ureB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kleanthous H;
                       4772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sussman I;
       CCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTAGG
                 Soman G,
Bhagat H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monath TP, Ackerman SK, Thomas WD, RA, Pappo J, Ermak T, Guirakhoo F,
                                                                                                                    H. pylori ureA + ureB gene locus in pORV214.
                                                                                                                                                                                                                                                                                                           "urease A subunit"
                                                                                                                                                                                                                                                                                                                                  subunit"
                                                                                                                                     Urease; ureA gene; ureB gene; vaccine;
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/note= "T7 terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 68-70; 98pp; English.
                                                                                                                                                                                                                                           function= "operator"
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                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                          urease genes"
complement (46. .67)
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2693. .2735
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'note= "BL1 primer"
                                                                                                                                                                                                                    the urease genes"
                                                                                                                                                       unidentified bacteriophage; T7 Chimeric.
                                                              AAT44351 standard; cDNA; 2735
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/*tag= f
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95US-00568122
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/*tag= e
/product= "u
                                                                                                                                                    Helicobacter; strain CPM630
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                                                                                                      (first entry)
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/*tag= 1
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06-DEC-1995;
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Weltzin RA,
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11-FEB-1997
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promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     926
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sequences coding for the urease A (AAW07193) and urease B (AAW07194) subunits of Helicobacter pylori clinical isolate CPM630. To obtain pORV214, a genomic DNA library of CPM630 was screened with anti-Helicobacter trasse antibody. A 17 kb S211 fragment from an isolated clone was subcloned into pUCI8 to give pSCP1. PCR primers (AAT44352-53) were used to amplify a 2.5 kb fragment from pSCP1, which was inserted into pGT24+ to give pORV214. The vector was utilised in the prodn. of recombinant, enzymatically inactive, multimeric urease in B. coli transformants for use in vaccines to treat or prevent Helicobacter infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 GTAGAAGCAGTAGCTTTGATTAGTGCCCATATTATGGAAGAAGAAGAGCTGGTAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 ACACTTTAAGAATAGGAGAATGAGATGAAACTCACCCCAAAAGGGTTAGATAAGTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 CTCCACTACGCTGGAGAATTGGCTAAAAAACGCAAAGAAAAAGGCATTAAGCTTAACTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTT----ATCAAGTAAGGAGACTCCCATGAAA----ATGAAAAAAAAAGAATATGTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 AAAATTTAACACAAGGAGTAATAGGTGAAACTCACACCCAAAGAGGCAAGAAAGTTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGAAGCCATTGCTTACATTAGTGCCCATATTATGGACGAAGCGCGCCGTGGAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 AAAAATGTTGGCGACAGACCGGTTCAAATCGGCTCACACTTCCATTTCTTTGAAGTGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u> aacagaagaarcriridgarirraacgcarringirgaraaraagaagaagaagaagaagaaa</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                      2; Length 2735;
                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                             Sequence 2735 BP; 875 A; 562 C; 635 G; 663 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           786; Indels
                                                                                                                                                                                                                                                                                                                                                                                Score 1021.4; DB 2
Pred. No. 1.3e-203;
0; Mismatches 786;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.5%;
Matches 1634; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2475 GTAACTICTAAACCAGCCAATAAAGTGAGCTTGGCGCAACTCTTTAGCATTTTCTAGG 2532
|||||| GAAGAAAAAGGCGATAAACGACAACTTCAGGATCAAAAGCTACTTGTCTAAATACACACATT
                                                                                                                                                                                                  2175 GGCGGATTCATTGCGTTAAGCCAAATGGGCGATGCGAACGCTTCTATCCCTACCCCACAA
                                                                                                                                                                                                                                                                                            2367 ACTTTTGTTTCCAAAGTCGCCTATGAAATGGCGTGAAAAGAAAAGCTGGGCTTAGAGCGC
                                                                                                                                                                                                                                                                                                             2415 ACTACTGCTCACATTGAAGTCAATCCTGAAACTTACCATGTGTTCGTGGATGGCAAAGAA
                                                                     2115 GCTGACTTGGTATTGTGGGAGTCCAGCATTCTTTGGCGTGAAACCCAACATGATCATCAAA
                                               2127 AACCCCGCTTTGACCCACGGCGTGAGCGAGTATATCGGCTCTGTGGAAGAGGGGCAAGATC
                                                                                                          GCCGACTTGGTGGTGGAATCCTGCCTTTTTTGGCGTAAAACCCCAAAATCGTGATCAAA
                                                                                                                                                                      GCCGGTATGGTCGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCACTCCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           se; UreA; UreB; vaccine; Helicobacter infection; UreI; shock protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site"
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/note= "ureA Shine-Dalgarno si
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/note= "UreB"
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heat shock pro
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                                                                                                                                        AAAATCCATGGCATTGGCAAGGCAGGAAACAAGGACATGCAAGATGGCGTAAGCCTTCAT 1226
                                                                                                                                                                                                                                              1227 ATGGTCGTGGGTGTGGGCACAGAAGCACTAGCAGGGGAAGGTATGATTATTACCGCTGGG 1286
                                                                                                                                                                                                                                                                                                          GGAATCGATTCACACCCCACTTCCTTTCTCCAACAATTCCCTACCGCTCTAGCCAAT 1346
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                                                                                           975 AGAGAAGGCATGAGCCAATCTAACAACCCTAGCAAAGAAGAAGGATTGGATTTAATCACT 1034
                                                                                                                        AACGCGATGATTATCGACTACACCGGGATTTACAAAGCCGACATTGGGATTAAAAACGGC 1166
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                                                                                                                                                                                                                                                        The sequence encodes urease UreA and UreB proteins, which are components of a novel immunogenic composition capable of inducing protective antibodies against Helicobacter infection. The composition may include the UreA or UreB proteins, a urease-associated heat shock protein (AAR74338-39) or the UreI protein (AAR74340). The composition is used to prepare a vaccine for humans or animals, especially against H. pylori and H. felis. Antibodies against the proteins may be used for treating Helicobacter infection, and primers/probes to the DNA sequence may be used for detection of Helicobacter infection. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                Immunogenic composition against Helicobacter infection - also gene fragment(s) and protein(s) from Helicobacter wrease gene cluster and heat shock protein(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2619 BP; 772 A; 569 C; 665 G; 613 T; 0 U; 0 Other;
                                              INST PASTEUR.
INST NAT SANTE & RECH MEDICALE
                                                                                            Suerbaum S, Ferrero R;
                                                                                                                                                                                                                                  Claim 10; Fig 3; 128pp; English
                 93WO-EP003259
                                                                                                                       WPI; 1995-200383/26.
P-PSDB; AAR74336, AAR74337.
                                                                                          Labigne A,
                                            (INSP)
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æ, 294 474 311 488 714 GTTAATGCTCCATTATGCGGGCAGATTGGCAGAAGGACGCTTGGCGCGTGGTGTGAAACT 131 CAACCAACCCGAAGCCATTGCTTACATTAGTGCCCATATTATGGACGAAGCGCGCCGTGG 354 Taccaatagaaattca-ataaggagtttaggatgaaactaacgcctaaagaactagacaa 71 GATGGACGCCGTAGCATCATCATGAAGTGGGGATTGAAGCTAACTTCCCCGATGG TGCCTTTAAAATTTAACACAAGGAGTAATAGGTGAAACTCACACCCAAAGAGGCAAGAAAA GTTCTTGTTATATTGCGGGCGAAGTGGCTAGAAAGCGCAAAGCAGAGGGCTTAAAAGCT TAATAAAAGCGTGGCGGATTTGATGCAAGAAGGCAGGACTTGGCTTAAAAAAGAAAATGT AATGCCCGGGGTGGGTAATATGGTTCCCGATCTAGGTGTAGAAGCCACCTTTCCTGATGG TACGAAACTIGTAACTGTGAATTGGCCCATCGAACCAGATGAGCACTTCAAAGCGGGCGA aaccaagcirigiaacrariccacriccgiagagaaaaradgccaaarragccccccggga 535 AGTGAAATTTGGTTGCGATAAAGACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACT AGCTAACAAGGCACTAAAATTCGATCGTGAAAAAGCCTATGGCAAACGCCTAGATATTCC 355 AAAAAAAACCGTTGCCCAGCTTATGGAAGAGTGCATGCACTTTTTGAAAAAAGATGAAGT AGTGAATAAGCTCTTGGACTTCGATCGCCCAAAAAGCTTTTGCAAACGCCTAGACATTGC GGT---CTTCTTAAAAATGAGGACATTACTATTAACGCCGGCAAAGAAGCCCATTAGCTT TGAGGTTACTAATGAAGGGCCTAAATCCTTGCATGTGGGTAGCCATTTCCACTTCTTTGA Gaps Length 2619; 42; Query Match 35.0%; Score 1008.8; DB 2; Length Best Local Similarity 66.2%; Pred. No. 5.5e-201; Matches 1634; Conservative 0; Mismatches 792; Indels 415 13 72 295 132 475 235 595

549 ATCTGGAACAGCGGTGCGCTTTGAACCCGGGGAGGAAAAAAAGTGTGGAACTCATTGACAT

CTCTGGCAACACGCTACGCATTGGGGCAGGACAAACCCGCAAAGTGCAGTTGATTCCTCT

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                                   céccécaaraacccarcraféctriraarrcrrregrécarceccaaccearecea
                                                                              ACGCCATAAAC----ATAAAGCGCTTGACAA------GGCGAAATCTCACGG
                                                                                                                   TGGTAAAAACTCGGCTTAAAACGCGCTAAAGAAAAAGGTTTTGGGTCTGTAAACTGCGG
                                                                                                                                                                                       ATATGTTTCTATGTATGGTCCCACTACGGGGATCGTGTTAGACTCGGCGACACTGATTT
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TGGTGGCAGTAAAAAGTGATTGGCATGAACGGGCTTGTGAATAACATCGCGGAT - - - GA
                                                                                                                                                          874 ATTT--ATCAAGTAAGGAGACTC------CCATGAAAATGA---AAAAACAAGA
                                                                                                                                                                                                                                         ATATIGTAAATACCTACGGACCCACCAAAGGCGATAAAGTGCGCTTAGGAGATACCGATCT
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A portion (AAT45680) of plasmid pILL205 (CNCM I-1355) comprises the Helicobacter felis structural urease gene encoding urease subunits A (AAM06729) and B (AAM06730). pILL205 was obtd. by examining the expression of urease activity by H. felis cosmid clones and identification of the H. felis genes required for urease expression when cloned in B. coll. The urease gene can be used to design probes for the detection of Helicobacter infection, or utilised in the prodn. of recombinant urease subunits for use in novel immunogenic compsns. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAACCAACCCGAAGCCATTGCTTACATTAGTGCCCATATTATGGACGAAGCGCGCCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunogenic compsn. contg. UreB and HspA antigens of Helicobacter for treatment and prevention of esp. H pylori infection, also new antibodies specific for these antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.0%; Score 1008.8; DB 2; Length 2619; 66.2%; Pred. No. 5.5e-201; tive 0; Mismatches 792; Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2619 BP; 772 A; 569 C; 665 G; 613 T; 0 U; 0 Other;
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                            1689 AAACACTGAAGCCGAGCACATGGACATGTTAATGGTGTGCCACCACTTGGATAAAGTAT 1748
                                                                                     CAAGGAAGATGTGCAGTTTCGAGGATTCGCCCCAAACTATCGCGGCTGAAGA 1808
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   13 TACCAATAGAAATTCA-ATAAGGAGTTTAGGATGAAACTAACGCCTAAAGAACTAGACAA
                                                                                                                                                                           295 CAACCAACCCGAAGCCATTGCTTACATTAGTGCCCCATATTATGGACGAAGCGCGCGTGG
                                                                                                                                                                                                                                                                                                                                     192 TAATAAAAGCGTGGCGGATTTGATGCAAGAAGGCAGGACTTGGCTTAAAAAAGAAAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; ureB gene; immunogen; vaccine; diagnostic; pylori; heat shock protein; HSP; chaperonin; pILL205; ss.
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Pred. No. 1.2e-200;
0; Mismatches 793; Indels 42;
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2469 GTTCTAGG 2476
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inducing an immune response against Helicobacter in a mammal, comprising mucosally administering to the mammal an attenuated Salmonella vector containing a nucleic acid molecule encoding a Helicobacter antigen, and parenterally administering to the mammal a Helicobacter antigen. Also included is an attenuated Salmonella vector comprising a nucleic acid molecule encoding a Helicobacter antigen. The Helicobacter antigen antenuated salmonella vector is a urease, a urease subunit, or its immunogenic fragment (encoded by the ureA and ureB genes). The mammal is at risk of
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infection. The attenuated Salmonella vector further comprises an htra or nirb promoter. The vector can be used in inducing an immune response against Helicobacter in a mammal. The vector can be used to treat Helicobacter infection. The vector and the method can be used to treat Helicobacter infection. The vector and the method can be used to treat Helicobacter infection. The vector and the method can be used to treat Helicobacter induced gastroduodenal diseases, including acute, chronic or atrophic gastricts, peptic ulcer diseases (e.g. gastric or duodenal closers), and gastric carcinoma. Attenuated Salmonella vector pHUR3 was constructed expressing Urea and Urea and including an B. coli AmpR gene. The present sequence represents the pHUR3 plasmid. NOTE: pHUR3 is represented by both ABES5112 and ABES5130, the peptides expressed by pHUR3 are shown in the sequence listing to be split between ABES5112 and ABES5130, the peptides being expressed by the one sequence, therefore all encoded peptides are cross-referenced to both sednences.

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Sequence 4824 BP; 1389 A; 1090 C; 1146 G; 1199 T; 0 U; 0 Other;

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850 268 AAACTCACCCCAAAAGAGTTAGATAAGTTGATGCTCCACTACGCTGGAGAATTGGCTAAA 148 208 388 448 269 GGACTCTTTAAAAACCAGATGATGATGGATGGATGGCGTGGCGAGCATGATCCATGAAGTG 328 GGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCCCATCGAA 508 568 445 AATGCAGGCAAAGAAGTAACCGAACTTGAGGTTACTAATGAAGGGCCTAAATCCTTGCAT 628 505 688 GCCTATGGCAAACGCCTAGATATTCCCTCTGGCAACACGCTACGCATTGGGGCAGGACAA 748 625 808 GAAAAATCCGTAGAATTGATTGACATTGGCGGTAACAGAAGAATCTTTGGATTTAACGCA 685 TTGGTTGATAGACAAGCAGACAACGAAAGCAAAAAATTGCTTTACACAGAGCTAAAGAG 745 896 802 ACCCGCAAAGTGCAGTTGATTCCTCTTGGTGGCAGTAAAAAAGTGATTGGCATGAACGGG --TAAACA----TAAAGCG cerectirircarececraaaaeceareaeaecaareaeaecaarraaeeaa <u> aaacecaaagaaaaagecarraaecrraaerrargaaecagraecrrraarragecc</u> GCCAATGGTAAATTAGTTCCTGGTGAGTTG---TTCTTAAAAAATGAAGACATCACTATC AACGAAGGCAAAAAAGCCGTTAAGCGTGAAAGTTAAAATGTTGGCGACAGACCGGTTCAA GTGGGTAGCCATTTCCACTTCTTTGAAGCTAACAAGGCACTAAAATTCGATCGTGAAAA ATCGGCTCACACTTCCATTCTTTGAAGTGAATAGATGCCTAGACTTTGACAGAGAAAA C----TIGACAAGGCG----AA---AICTCACGGAITT---AICAAGIAAGGAGACTCCC AACGAAATTAGGACTATAATCCCATTGCCTTTAAAATTTAACACAAG-GAGTAATAGGTG AAATGAATCTGACGTACACAGCAATTTAGATATTAATCATCCACAGGAGAGATCTCCATG <u>AAACTCACACCCAAAGAGCAAGAAAGTTCTTGTTATTATTATGCGGGCGAAGTGGCTAGA</u> CATATTATGGACGAAGGGCGCGTGGAAAAAAAAAACCGTTGCCCCAGCTTATGGAAGAGTGC 509 CCAGATGAGCACTTCAAAGCGGGCGAAGTGAAATTTGGTTGCGATAAAGACATCGAGCTC actrircegraaacecriagacatregeaecegeacacegeraacarrirgaecereeceaa **AAGCGCAAAGCAGAGGGCTTAAAGCTCAACCAACCGAAGCCATTGCTTACATTAGTGCC** Gaps 39; Length 4824; Ouery Match 34.9%; Score 1005.8; DB 5; Length Best Local Similarity 65.8%; Pred. No. 2.8e-200; Matches 1640; Conservative 0; Mismatches 812; Indels CTIGIGAATAACATCGCGG---ATGAACGCCA-150 149 389 449 329 389 446 206 689 49 526 989 746 59 209 89 269 329 209 569 629 809 851

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1613 1853 1013 1073 1286 ACCGGTCCTGCTGATGGCACTAATGCGACTACTATCACTCCAGGCAGAGAAATTTAAAA 1345 1346 regarecreasaccecreaagaararrerargaarrracerrrecraagecraaaceraa 925 1466 CACGAAGACTGGGGCACCACTCCTGCAATCAATGATGCGTTAGATGTTGCGGACAAA GAAGAACTTAAATTTTGGCGCGGGTAAAACTATCCGTGAGGGTATGGGTCAGAGCAATAGC 1226 TCACCCCAACAAATCCCTACAGCTTTTGCAAGCGGTGTAACAACCATGATTGGTGGTGGA cercaaaccarreceecreaaeacaerrrecareacareseearrrrereaareaceaer 1134 ATTTACAAAGCCGACATTGGGATTAAAAACGGCAAAATCCATGGCATTGGCAAGGCAGGA ACAGGTCCTGTAGATGGCACGACTACTATCACTCCGGGCAAATGGAACTTGCAC 1614 TACGATGTGCAAGTTTGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATGAC ggacacrcaccrcargrrarcaccargecagecagecrcaararreraccerceaee CCTGATGAAAACACCCTAGATTTAGTCATCACTAAACGCGATGATTATCGACTACACCGGG TCTCCACAACAATTCCCTACCGCTCTAGCCAATGGCGTTACAACCATGTTTGGAGGCGGC 1406 GCTTCTAACGATGCGAGCTTAGCCGATCAAATTGAAGCCGGTGCGATTGGCTTTGCAATT ACCCTAAATGCAATGAACGGGCGCGCCATCCATGCCTACCACATTGAGGGAGCGGGGGGA 1646 GGACACGCTCCTGATATTATTAAAGTAGCCGGTGAACACAACACATTCTTCCCGCTTCCACT ACCCCCACTATTCCCTATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGACA 1854 TGCCACCACCTAGACAAACGCATCCGCGAGGATTTACAATTTTCTCAAAGCCGTATCCGC TGCCACCACTTGGATAAAAGCATTAAAGAAGATGTTCAGTTCGCTGATTCAAGGATCCGC CCCGGCTCTATCGCGGCTGAAGATGTGCTCCATGATATGGGTGTGATGACGATGACAAGC GTGCGCTTAGGAGATACCGATCTTTGGGCAGAAGTAGAACATGACTATACCACCTATGGC grgagarriggeccarracacerrearcecrgaagragaacargacracaccarrrargec ccragcaaagagriggariraarrarcacraacgcrrraarcgrggarracaccgg 1194 AACAAGGACATGCAAGATGGCGTAAGCCCTCATATGGTCGTGGGTGTGGGCACAGAAGCA CTAGCAGGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACACCCCCTT rradecederaadgringanegraacogerografingaeacaeacaeacricarr 1434 CGCATGTTGCGCGCAGCAGAAGAGTATTCTATGAATGTGGGCCTTTTTGGGCAAAGGCAAT CATGAAGACTGGGGCACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAA ATGAAA----ATGAAAAACAAGAATATGTAAATACCTACGGACCCACCAAAGGCGATAAA 1586 1314 1734 1794 1706 1766 1826 1014 1074 986 1046 1106 1254 1166 1374 1674 1914 1554

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TCGGATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTGCG 2033
                                                                                                                               CGCATTAAGCGCTACATCTCCAAATACACTATCAACCCCGCTTTGACCCACGGCGTGAGC 2153
                                                                                                                                                                                              GAGTATATCGGCTCTGTGGAAGAGGGCAAGATCGCCGACTTGGTGGTGTGGAATCCTGCC 2213
                                                                                                                                                                                                                              GAGTATGTAGGTTCAGTAGAAGTGGGCAAAGTGGCTGACTTGGTATTGTGGAGTCCAGCA 2125
                                                             GATAAGAATAAAAAAGAATTTGGTAAGCTTCCTGAAGATGGCAAAGATAACGATAATTTC
                                                                                                                                                   2186 GGCGATGGAACGCTTCTATCCCTACCCCACAACCGGTTTATTACAGAGAAATGTTCGCT
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in a mammal, comprising microsally administering to the mammal an attenuated Salmonella vector containing a mucleic acid molecule encoding a Helicobacter antigen, and parenterally administering to the mammal and Helicobacter antigen. Also included is an attenuated Salmonella vector comprising a nucleic acid molecule encoding a Helicobacter antigen. The Helicobacter antigen is a urease, a urease subunit, or its immunogenic fragment (encoded by the urea, and urea genes). The mammal is at risk of having but does not have Helicobacter infection or has a Helicobacter or infection. The attenuated Salmonella vector further comprises an hirh or in a promoter. The vector can be used in inducing an immune response against Helicobacter in a mammal. The vector can be used to treat thelicobacter infection. The vector and the method can be used to treat Helicobacter infection. The vector and the method can be used to treat thelicobacter induced gastroducdenal diseases, including acute, chronic constructed expressing Urea and the method can be used to treat the present sequence represents the pHUR3 plasmid. NOTE: pHUR3 was constructed expressing Urea and Arbelland Salmonella vector pHUR3 and Salmonella vector pHUR3 are shown in the sequence listing to be split between ABB55112 and ABB5513. A BB55132 and Salmonella supprides being expressed by the one constructed to both the peptides are cross-referenced to both the construction and processed by the one construction and processed processed by the construction and processed processed processed by the construction and processed p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to inducing an immune response against Helicobacter in a mammal, comprising mucosally administering to the mammal an
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                                                                                                                                                                                                                                                                                                                             Inducing an immune response against Helicobacter in mammals, useful for
treating Helicobacter induced gastroduodenal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 AAACTCACACCCAAAGAGCAAGAAAAGTTCTTGTTATATTATGCGGGCGAAGTGGCTAGA
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                                                                                                                                             P-PSDB; AEB55113, AEB55114, AEB55115, AEB55116, AEB55117, AEB55118, AEB55119, AEB55121, AEB55122, AEB55123, AEB55125, AEB55125, AEB55125, AEB55125, AEB55125, AEB55132, AEB55132, AEB55134, AEB55137, AEB551318, AEB551318, AEB551318, AEB551318, AEB551319, AEB55140,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4824 BP; 1389 A; 1090 C; 1146 G; 1199 T; 0 U; 0 Other;
                                                          Freeman D;
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 1; 63pp; English
                                                          Londono-Arcila P,
                                                                                                                 2001-343379/36
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Matches 1640; Conserv
(ORAV-) ORAVAX INC
                                                          Kleanthous H,
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Qy 1614 TACK Db 1526 TACK	Qy 1674 ACC Db 1586 ACT	Qy 1734 GGA(Db 1646 GGA(Qy 1794 ACC	Qy 1854 TGC Db 1766 TGC	1914	1974	2034	2094	2154 2066	2214	2274	2334 2246			Oy 2514 AAA. Db 2426 GAA.		RESULT 13 AAQ12485 ID AAQ12485 sta: XX
	n 80 u	748 .	. 808 808 808	850 745	808 805	ATGAAAATGAAAAAACAAGAATHIGTAAATACCTACGGACCCCCCAAAGGCGATAAA 953	GTGCGCTTAGGAGATACCGATCTTTGGGCAGAAGTAGAACATGACTATACCACCTATGGC 1013	Qy Qy GAAGAACTTAAATTTGGCGCGGGTAAAACTATCCGTGAGGGTATGGGTCAGAGCAATAGC 1073 D	CCTGATGAAAACACCCTAGATTTAGTCATCAACGCGATGATTATCGACTACACGGG 1133	ATTTACAAAGCCGACATTGGGATTAAAAACGGCAAAATCCGTGGCATTGGCAAGGCAGGA 1193	OY AACAAGGACATGCAAAGAGCGTAAGCCCTCATATGGTCGTGGGGTGTGGGGCACAGAAGGA 1253	1313 1225	TCTCCACAACAATTCCCTACGGCTCTAGCCATGGCGTTACAACCATGTTTGGAGGGGGC 1373	ACAGGTCCTGTAGATGGCACGAATGCGACTACTATCACTCCGGGCAAATGGAACTTGCAC 1433	CGCATGTTGCGCGCAGCAGAAGAGTATTCTATGAATGTGGGCCTTTTTGGGCAAAGGCAAT 1493	AGCTCTAGCAAAAACAACTTGTAGAACAGTAGAAGCGGGGGCGCGATTGGTTTTAAATTG 1553	CATGARGACTGGGGCACAAGTGCGATCGATCGATCGATCGAGCGTGGCGAGATGAA 1613 RESULT
569 AATG	629 GTGG	000 POC TITLE OF THE PO	749 ACCC 626 GAAA	809 CTTG 686 TTGG	851 C 746 CGTG	897 ATGA 806 ATGA	954 GTGC 866 GTGA	1014 GAAG 926 GAAG	1074 CCTG 986 CCTA	1134 ATTT 1046 ATTT	1194 AACA 1106 AACA	1254 CTAG 1166 TTAG	1314 TCTC 1226 TCAC	1374 ACAG 1286 ACCG	1434 CGCA 1346 TGGA	1494 AGCT 1406 GCTT	1554 CATG 1466 CACG

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RESULT 13 AAQ12485 ID AAQ12485 standard; DNA; 2767

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA is a 2.7 kb TaqI fragment encoding the A and B subunits of H. pylori (previously C. pylori) urease, i.e. the 66 and 31 kb antigens. From the sequence, probes and primers can be designed for the amplification (by PCR) of the gene, to produce a prods. common to all H. pylori strains so far tested and which do not occur in other ureases and can therefore be used as a specific indication of the presence of H. pylori. H. pylori (previously C. pylori) is strongly implicated in the pathogenesis of gastritis and duodenal and peptic ulceration in man. The primers probes can be used for the detection of H. pylori DNA in gastric mucosa, saliva or faecal samples to provide an early diagnosis of infection. See also AAQ12434-Q12486. (Updated on 27-AUG-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATATTATTATGCGGGGAAGTGGCTAGAAAGCGCAAAGCAGGGGCTTAAAGCTCAACCAA 301
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                                                                                                                                                                                                                                                                                                                                                                                        Oligo:nucleotide(s) specific for Heliobacter pylori - used as probes primers to detect H pylori infection, in diagnosis of gastritis, and duodenal and peptic ulceration.
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                                                   DNA encoding A and B subunits of H. pylori urease
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0; Mismatches 792;
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64. .717
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/note= "66 kD"
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/*tag= b
/label= subunit B
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                                                                                                                                                                                                      /note= "31 kD
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                     (revised)
(first entry)
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Matches 1627; Conservative
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                                                                                              Helicobacter pylori
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AAQ12485
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                                                                                                                                                                                                                        CTTGTAACTGTGAATTGGCCCCATCGAACCAGATGAGCACTTCAAAGCGGGCGAAGTGAAA
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                                                                                                                                                     GGCGTGGCAAGCATGATCCATGAAGTGGGTATTGAAGCGATGTTTCCTGATGGGACCAAA
                                                                                                                                                                                                                                                                                                                                                         542 TTTGGTTGCGATAAAGACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACTTGAGGTT
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                                                                                   GGGGTGGGTAATATGGTTCCCGATCTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAA
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                                                                                                      GAAGCGGGCGCGATTGGTTTTAAATTGCATGAAGACTGGGGCACAACACCCAAGTGCGATC 1586
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               ATCACTCCAGGTAGAAGAAATTTAAAATTCATGCTCAGAGCGGCTGAAGAATATTCTATG
                                                                    AACTITIGGITICTIGGCIAAAGGIAACGCTICTAACGAIGCAAGCTIAGCCGAICAAATI
                                                                                                                                                                                                                          GAAGATGGCAAAGATAACGATAATTTCCGCATTAAGCGCTACATCTCCAAATACACTATC
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                                           AATGTGGGCTTTTTGGGCAAAGGCAATAGCTCTAGCAAAAAAACAACTTGTAGAACAAGTA
                                                                                                                        GCAGAACACTTAGACATGCTCATGACATGCCACCACCTAGACAAACGCATCCGCGAGGAT
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arricural gene and at least one urease accessory gene. The nucleic acid molecule is chosen from urea, urease accessory gene. The nucleic acid molecule is chosen from urea, ureB, ureF, ureG, ureH and ureI. The invention also relates to an isolated protein encoded by the nucleic acid, a vaccine for preventing onset of disease in mammals infected by H. bizzozeronii comprising a nucleic acid and a carrier, and an isolated antibody or its binding portion raised against the nucleic acid. The nucleic acids, proteins and antibodies are useful for vaccinating mammals against onset of disease caused by infection of H. bizzozeronii, which involves administering the sequences. The sequences are useful for detecting H. bizzozeronii in a sample of tissue or body fluids which involves providing a nucleic acid as an antigen, providing an antibody, or providing a nucleic acid as an antigen, providing an antibody or providing an antibody or providing any reaction which indicates that H. bizzozeronii is present in the sample. This sequence represents H. bizzozeronii ureB DNA.
2377 ACTACCGCTCACATTGAAGTCAATTCTGAAACTTACCATGTGTTCGTGGATGGCAAA-GA 2435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule having urease gene cluster, and conferring on Helicobacter bizzozeronii ability to produce urease, useful as vaccine for preventing disease in mammals infected by H.bizzozeronii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule conferring on Helicobacter bizzozeronii an ability to produce urease, where the nucleic acid molecule is a urease gene cluster comprising at least one urease
                                                                                                                                      2436 AGTAACTCTAAACCAGCCAATAAAGTGAGCTTGGCGCAACTCTTTAGCATTTTCTAGG 2493
                                                                                2547 TGCACCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTAGG 2604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    urease structural gene;
Helicobacter bizzozeronii infection;
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1. .1710
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(SIMP/) SIMPSON K W.
(ZHUJ/) ZHU J.
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ABA00816 standard; cDNA; 1719
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                                                                                                                                                                                                                                   AAAGCCGACATTGGGATTAAAAACGGCAAAATCCATGGCATTGGCAAGGCAGGAAACAAG 1199
                                                                                                                                                                                                                                                                                                                                    GGGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACACCCCACTTCCTCCA 1319
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                                     AAAATGAAAAAACAAGAATATGTAAATACCTACGGACCCACCAAAGGCGATAAAGTGCGC
                                                            <u> AAAATCTCTCGAAAAGAATATGTTTCTATGTATGGACCCACTACGGCGATAAAGTGAGA</u>
                                                                                    TTAGGAGATACCGATCTTTGGGCAGAAGTAGAACATGACTATACCACCTATGGCGAAGAA
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            0; Mismatches 477; Indels
  Pred. No. 8.3e-187;
Best Local Similarity 72.0%;
Matches 1227; Conservative
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                                                                                                                                                                                                                                                                                                                                   <u> aacaaaaaaaarrrrgercecrrecergagaaaaaggcgaraargacaacrrecgcare</u>
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                                                                                                                                                                   This sequence encodes H. felis urease B. This sequence was used in the method of the invention for raising an immune response in an animal. The method comprises administering to the animal a composition comprising a carrier and an antigen bound to a targeting moiety which binds to at least one receptor present in circulatory vessels in Gut Associated Lymphoid Tissue (GALT). The method is useful for raising an immune response in an animal against antigens from Salmonella, Cholera, Helicobacter pylori, HIV, Candida, P. gingivalis, gut barasites, gut associated toxins, gut hormones, gut hormone receptors or gut associated cancers. The method is useful for raising both mucosal and systemic immunity against any antigen used in the composition
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                                                                             Raising an immune response in an animal by administering composition comprising carrier and antigen bound to targeting moiety which binds receptor present in circulatory vessels in Gut Associated Lymphoid
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Pred. No. 9.1e-179;
0; Mismatches 501; Indels 0;
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COUNCIL QUEENSLAND INST MEDICAL RES
                                                                                                                                              Disclosure; Page 27-28; 45pp; English
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Best Local Similarity 70.6%;
Matches 1203; Conservative
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1: /EMC Celerra SIDS3/ptodata/2/ina/1 COMB.seq:*
2: /EMC Celerra SIDS3/ptodata/2/ina/5 COMB.seq:*
3: /EMC Celerra SIDS3/ptodata/2/ina/6A COMB.seq:*
4: /EMC Celerra SIDS3/ptodata/2/ina/6A COMB.seq:*
5: /EMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*
6: /EMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*
7: /EMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*
8: /EMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*
9: /EMC Celerra SIDS3/ptodata/2/ina/PP COMB.seq:*
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                        GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-431-90A-1

US-09-55-884-1

US-09-55-884-1

US-09-55-884-1

US-09-55-884-1

US-09-543-681A-1857

US-09-543-681A-1857

US-08-687-513-1

US-08-687-613-1

US-08-487-4294-22

US-08-95-171E-22

US-08-95-171E-25

US-08-95-171E-25

US-09-328-35-1786

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US-09-453-702B-258
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Maximum Match 100%
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1167	AAAATCCATGGCATTGGCAAGGCAGGAACAAGGATGCCATGCAAGATGGCGTAAAGTCATCA	ò	2247 GGCC
1095	AAAATGGCTGGCATTGGTAAAGGGGGGTAACAAAGGACATGCAAGATGGCGTTAAAAACAAT	q	2175 GGCC
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      78 ACACTTTAAGAATAGGAGAATGAGATGAAACTCACCCCAAAAGAGTTAGATAAGTTGATG 137
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                                                                                                                            138 CTCCACTACGCTGGAGAATTGGCTAAAAAACGCAAAAAAGGAAAAAGGCATTAAGCTTAACTAT
                                                                                                                                                                                                  302 CCCGAAGCCATTGCTTACATTAGTGCCCATATTATGGACGAAGCGCGCCGTGGAAAAAA
                                                                                                                                                                                                                                                                  198 GTAGAAGCAGTAGCTTTGATTAGTGCCCATATTATGGAAGAAGAAGAGGGGGAGGTGGTAAAAAG
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                                                                      TTATATTATGCGGCGAAGTGGCTAGAAAGCGCAAAGCAGAGGCCTTAAAGCTCAACCAA
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                                 2235 CCGGTTTATTACAGAGAAATGTTCGCTCATCATGGTAAAGCTAAATACGATGCAAACATC 2294
                                                                                                 ACTITITGTITCCAAAGTCGCCTATGAAAATGGCGTGAAAGAAAAGCTGGGCTTAGAGCGC 2426
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                                                                                                                                                                                                                                 2355 CAAGTGTTGCCGGTAAAAATTGCAGAAATATCACTAAAAAAGACATGCAATTCAACGAC 2414
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                                                                                                                                                                                                                                                                                                                                                                                                                             2415 ACTACTGCTCACATTGAAGTCAATCCTGAAACTTACCATGTGTTCGTGGATGGCAAAGAA 2474
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TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05800
FILING DATE: 23-APR-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.5%; Score 1021.4; DB 7;
66.5%; Pred. No. 6.6e-244;
vative 0; Mismatches 786;
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/02001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9605800 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,122
FILING DATE: 06-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,041
FILING DATE: 28-APR-1995
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 66.5
Matches 1634; Conservative
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COUNTRY: USA
ZIP: 02110-2804
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PCT-US96-05800-1
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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sterrero, Richard L.
APPLICANT: Sterrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLLYPEPTIDES
NUMBER OF SEQUENCES 44
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
2367 ACTITITGITICCAAAGICGCCTAIGAAAAIGGCGTGAAAGAAAAGCIGGGCTIAGAGCGC 2426
                                                                                                                                                                                                                       AAAACGGCAAAAATCACCGTCGATCCGAAAACCTTCGAGGTCTTTGTAGATGGCAAACTC 2546
                                                                                                                                                                                                                                                                          2415 ACTACTGCTCACATTGAAGTCAATCCTGAAACTTACCATGTGTTTCGTGGATGGCAAAGAA 2474
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                                                ACTITITICITCITCAAGCGCTTATGACAAGGCATTAAAGAAGAATTAGGACTTGAAAGA
                                                                                                          CAAGITCTACCGGTCAAAAACTGCCGTAACATCACCAAGAAAGACTTCAAGGTCAACGAC
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ZIP: 20005-3315

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIPICATION NUMBER: US/08/447,177
PILING DATE: 19-MAY-1995
CLASSIPICATION ADATA:
APPLICATION NUMBER: US 08/447,177
PILING DATE: 19-MAY-1995
CLASSIPICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
ATTORNEY AGBNT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION: 1000, 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08467822
Patent No. 5843460
GENERAL INFORMATION:
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TELEPAX: (202) 408-4400
INFORMATION FOR SEG ID NO: 19:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: n
LOCATION: 3
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                                                                                                                                                                                  TACCAATAGAAATTCA-ATAAGGAGTTTAGGATGAAACTAACGCCTAAAGAACTAGACAA 71
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                                                                                                                                                                                                                                                                                                           AAAAAAACCGTTGCCCAGCTTATGGAAGAGTGCATGCACTTTTTGAAAAAAGATGAAGT
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                                                                                                                                   42;
                                                                                                           Length 2619;
                                                                                                         Query Match 35.0%; Score 1008.8; DB 2; Length Best Local Similarity 66.2%; Pred. No. 8.9e-241; Matches 1634; Conservative 0; Mismatches 792; Indels
OTHER INFORMATION: /standard_name= "Shine-Dalgarno OTHER INFORMATION: sequence."
                     FEATURE:

NAME/KEY: misc_feature

LOCATION: 756..759

OTHER INFORMATION: /standard_name= "Shine-Dalgarno";

OTHER INFORMATION: sequence."
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۾	1269	TGCGACCACCATCACTCCCGGACGCGCTAATCTAAAAAGTATGTTGCGTGCAGCCGAAGA 1328
<u>></u>	1457	GTATTCTATGAATGTGGGCTTTTTTGGGCAAAGGCAATAGCTCTAGCAAAAAACAACTTGT 1516
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۲ ۸	6	CGCCATCCATGCCTACCACATTGAGGGAGGGGGGGGGACACTCACCTGATGTTATCAC 1756
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>	81	187
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Д	1749	0
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Ω.	1869	192
>-	2057	TAAGCTICCTGAAGATGGCAAAGATAACGATAATTICCGCATTAAGCGCTACATCTCCCAA 2116
Δ.	1929	19
>-	2117	ATACACTATCAACCCCGCTTTGACCCACGCGTGAGCGAGTATATCGGCTCTGTGGAAGA 2176

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874 ATTT--ATCAAGTAAGGAGACTC------CCATGAAAATGA---AAAAACAAGA
                                                                                                                   MOLECULE TYPE: DNA (genomic) FEATURE:
   TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2619 base pairs
                                                                                                                                                  NAME/KEY: misc feature LOCATION: 31..36 OTHER INFORMATION: /sta
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 66.2
Matches 1634; Conservative
                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                       linear
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Sequence 19, Application US/08432697

Patent No. 6248330

GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENTICOMPOSITIONS AGAINST
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                      2168
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TGGCAAAGAGGTAACCTCTAAAGCAGCAGATGAATTGAGCCTAGCGCAACTTTATAATTT 2468
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                                                                                                                                                                                                                      CACCCCTCAGCCCGTCTATTACCGTGAAATGTTTGGACACCATGGGAAAAAACAAATTCGA 2228
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                                                                                                                                                    2109 GATTATTAAGGGCGGATTTATTGCGCTCTCTCAAATGGGCGATGCCAATGCGTCTATTCC
                                                                                                                                                                                       CACTCCCCAACCGGTTTATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTTGA
                                                                                                                                                                                                                                                       CTTAGAGCGCCAAGTTCTACCGGTCAAAACTGCCGTAACATCACCAAGAAAAAGACTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PR Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1300 I Street, N.W.
CITY: Washington
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 AACCAAGCTIGIAACTATCCACACTCCGGTAGAGGATAATGGCAAATTAGCCCCCGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 CAACCAACCCGAAGCCATTGCTTACATTAGTGCCCCATATTATGGACGAAGCGCGCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 GGT---CTTCTTAAAAATGAGGACATTACTATTAACGCCGGAAAGAAGCCATTAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 GAAAGTGAAAATAAAGGCGATCGTCCTGTGCAGGTGGGATCACATTTCCACTTCTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                655 AGCTAACAAGGCACTAAAATTCGATCGTGAAAAAGCCTATGGCAAACGCCTAGATATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489 AGTGAATAAGCTCTTGGACTTCGATCGCGCAAAAGCTTTTGCAAACGCCTAGACATTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 CAATTACACCGAAGCGGTCGCGCTCATTAGCGGCCGTGTGATGGAAAAGGCGCGCGTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 TAATAAAAGCGTGGCGGATTTGATGCAAGAAGGCAGGACTTGGCTTAAAAAGAAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 TACGAAACTTGTAACTGTGAATTGGCCCATCGAACCAGATGAGCACTTCAAAGCGGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 AGTGAAATTTGGTTGCGATAAAGACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     715 CTCTGGCAACACGCTACGCATTGGGGCAGGACAAACCCGCAAAGTGCAGTTGATTCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            775 TGGTGGCAGTAAAAAGTGATTGGCATGAACGGGCTTGTGAATAACATCGCGGAT---GA
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                     Length 2619;
                                                                                                                                                                                                                                                                                                      Indels
                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 756.759
OTHER INFORMATION: /standard_name= "Shine-Dalgarno
OTHER INFORMATION: sequence."
/standard_name= "Shine-Dalgarno
sequence."
                                                                                                                                                                                                                                                35.0%; Score 1008.8; DB 3; 66.2%; Pred. No. 8.9e-241; tive 0; Mismatches 792;
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Sequence 19, Application US/08466248

Sequence 19, Application US/08466248

Patent No. 6258359

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastien

APPLICANT: Thiberge, Jean-Michel

TITLE OF INVENTION: HELICANCER INFECTION, POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

STREET: 1300 I Street, N.W.

CITY: Washington

STREET: D.C.
CCAACTCCATGACATGGGGATCTTTTCTATCACCCAGCTCCGACTCTCAGGCTATGGGACG 1868
                                                                                                                                                                                                      ATACACCCATCAACCCCGGGATCGCGCATGGGATTTCTGACTATGTGGGCTCTGTGGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2289 GCTAGATCGCGCGGCACCGCCAGTGAAAACTGTCGCAATATCACTAAAAAGGACCTCAA
                                                         GCGCTTGAAAGGGGAAAAAGGCGATAACGACAACTTCCGCATCAAACGCTACATCTCTAA
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                                                                                                      2057 TAAGCTTCCTGAAGATGGCAAAGATAACGATAATTTCCGCATTAAGCGCTACATCTCCAA
                                                                                                                                                                              ATACACTATCAACCCCGCTTTGACCCACGGCGTGAGCGAGTATATCGGCTCTGTGGAAGA
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                                                                                                                                                                                                                                                                                      2109 GATTATTAAGGGCGGATTTATTGCGCTCTCTCAAATGGGCGATGCCAATGCGTCTATTCC
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                                     TGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAGAATTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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2469 GTTCTAGG 2476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1629 AATGGCAGGGGAATTTAACATTCTACCCGCCTCTACTAACCCGACCATTCCTTTCACCAA 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1689 AAACACTGAAGCCGAGCACATGGACATGTTAATGGTGTGCCACCACTTGGATAAAAGTAT 1748
                                                                                                                                                          908
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                                                                                                                                                                                                                                909 TAAAACTATCCGTGATGGGATGAGTCAAACCAATAGCCCTAGCTCTTATGAATTAGATTT 968
                                                                                                                                           TTGTGAAGCGACTAAAGATAAACAATAAGGAAAAAACCATGAAAAAGATTTCACGAAAAGA
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        429 GAAAGIGAAAAITAAAGGCGAICGICCIGIGCAGGIGGGAICACAITIICCACIITIIGA 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "Shine-Dalgarno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
COCATION: 756..759
OTHER INFORMATION: /standard_name= "Shine-Dalgarno
OTHER INFORMATION: sequence."
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2619 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 31...36
OTHER INFORMATION: /st.
OTHER INFORMATION: seq
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Matches 1634; Conservative
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TITLE OF INVENTION: Use of salmonella vectors for ; TITLE OF INVENTION: Vaccination against helicobacter infection ; FILE REFERENCE: 06132/060001 ; CURRENT APPLICATION NUMBER: US/09/431,705 ; CURRENT PILING DATE: 1999-11-01 ; NUMBER OF SEQ ID NOS: 52 ; SOPTWARE: PastSEQ for Wir.3 ; SEQ ID NO 1 ; LENGTON 1
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                                                                                                                                                                                                                                                                                     OTHER INFORMATION: includes sequences from Helicobacter pylori, OTHER INFORMATION: Salmonella typhimurium, and Escherichia coli NAME/KEY: CDS
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ORGANISM: Artificial Sequence
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US-09-431-705-1 Sequence 1, Application US/09431705 Patent No. 6585975 GENERAL INFORMATION: APPLICANT: Kleanthous, Harold APPLICANT: Londono-Arcila, Patricia

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                                                                 329 GGTATTGAAGCGATGTTTCCTGATGGGACTAAACTCGTAAACCGTGCATACCCCTATTGAG
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                                         GGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCCCATCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: includes sequences from Helicobacter pylori,
OTHER INFORMATION: Salmonella typhimurium, and Escherichia coli
                                                                                                                                                                                            APPLICANT: Kleanthous, Harold
APPLICANT: Londono-Arcila, Patricia
APPLICANT: Londono-Arcila, Patricia
APPLICANT: Freeman, Donna
TITLE OF INVENTION: Use of salmonella vectors for
TITLE OF INVENTION: vaccination against helicobacter infection
FILE REFERENCE: 06132/060001
CURRENT APPLICATION NUMBER: US/09/431,705
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 52
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                                    2486 AGCTTGGCGCAACTCTTTAGCATTTTCTAGG 2516
2574 CCTCTAGCCCAGCGCTACACTTTCTTCTAGG 2604
                                                                                                                                                                                                                                                                                                                                                              SEQ ID NOS: 52
FastSEQ for Windows Version 4.0
                                                                                                                                   Sequence 19, Application US/09431705
Patent No. 6585975
GENERAL INFORMATION:
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LOCATION: (389
NAME/KEY: CDS
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2574 CCTCTAGCCCAGCGCTACACTTTCTTCTAGG
                                                                                                                                                                                                                                                                    Sequence 8, Application US/07732242C Patent No. 5298399 GENERAL INFORMATION:
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REGISTRATION NUMBER: 17081
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELECHONE: (212)972-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TYPE: NUCLEIC ACID
STRANDEDNESS: both
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                           1406 GCTTCTAACGAIGCGAGCTTAGCCGATCAAATTGAAGCCGGTGCGATTGGCTTTGCAATT 1465
                                                                                                                                                                                              CATGAAGACTGGGGCACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAA 1613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGATTCTAACGCGTCTGTGCCCCACTCCCCAACCGGTTTATTACCGCGAAATGTTTGGG 2333
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                                 AATGGCGTGAAAGAAAAGCTGGGCTTAGAGCGCCAAGTTCTACCGGTCAAAAACTGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 ACTIMAMAINGGAGGITATCCATGAACIGACTTCACGTGAAATGGAAAAGCTCATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 ATTTAACACAAGGAGTAATAGGTGAAACTCACACCCAAAGAGCAAGAAAAGTTCTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 TATTATGCGGCGAAGTGGCTAGAAAGCGCAAAGCAGAGGGCTTAAAGCTCAACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                       APPLICANT: Uozumi, Takeshi; Masaki, Haruhiko;
APPLICANT: Hidaka, Makoto; Nakamura, Akira;
APPLICANT: Hidaka, Makoto; Nakamura, Akira;
APPLICANT: Madada, Michihisa; Yoneta, Yasuo
ITITLE OP INVENTION: Gene of Urease
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
ADDRESSEE: Frishauf, Holtz, Goodman & Woodward, P.C.
STREET: 600 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                          STREFI: COUNTY: New York
STATE: New York
COUNTRY: USA
ZIP: 10016-2088
COMPUTER READABLE FORM:
MEDIUM TREE: 3.5 inch, 0.72mb
COMPUTER: IBM PC COMPATIBLE (NEC PC-9801 RX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%; Score 667.4; DB 2; ilarity 59.0%; Pred. No. 1.3e-155; Conservative 0; Mismatches 951;
2604
                                             2516
                                             2486 AGCTTGGCGCAACTCTTTAGCATTTTCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII Form
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,242C
FILING DATE: 19910718
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: JPN 2-210178
FILING DATE: 10-AUG-1990
ATTORNEY/AGENT INFORMATION:
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1857 2240 2300 2277 2360 2180 2217 2480 TTATTTTGAGGTGAGAAAAACATGATGGTTGAAAAAGTAGTCG 2720 AGATGTGCTCCATGATATGGGTGTGATCGCGATGACAAGCTCGG CCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAATACG Aggajagriacaagajagaanggngnggagagagagartrcgrg CATCCGCGAGGATTTACAATTTTCTCAAAGCCGTATCCGCCCCG 3GCTTAGAGCGCCAAGTTCTACCGGTCAAAAACTGCCGTAACA TTCTTCTAGGCACAATGCCCCCTTTGGGGGCCAGGTTATTTAG SCGCCCCATCCATGCCTACCACATTGAGGGAGCGGGTGGAGGAC ATCGTGATCAAAGGCGGTATGGTGGTCTTCTCTGAAATGGGCG CATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGCC SCGTGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTGCGGATA **IGGTAAGCTTCCTGAAGATGGCAAAGATAACGATAATTTCCGCA** GAGGGCAAGATCGCCGACTTGGTGGTGTGGGAATCCTGCCTTTT GACACCAGCATCACTTTTGTTTCCAAAGTCGCCTATGAAAATG AAGTTCAACGACAAAACGGCAAAAATCACCGTCGATCCGAAAA GATGGCAAACTCTGCACCTCTAAACCCACCTCGCAAGTGCCTC GACGGTCAATTAGTGACATGTGAACCGGCAGAAATCGTCCCTA

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563682 TGGCCCTGCTGATGGTACACACGCAACCACTTGTACCCCTGGCGCATGGTATATGGAACG 563623
                                                                        564701 ATATGGCGCAACACTTTTAACCGTTGATGATGTCATGGAAGGTGTGGGGAAATGGTTCA 564642
                                                                                                                                                                                                                                                                   564581 AATCAGATAACCGWAGGGTGGGCTTTAGCCCACAAAATAAAAATATCAATGGTGGGCTAA 564522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGATCGTGAAAAAGCCT---ATGGCAAACGCCTAGATATTCCCTCTGGCAACACGCTA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            564461 TATTCTCGCTAATGTCGCCAGAAAACCGTAAAAATCGAAGTAACAAATTCAGGCGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564281 ACCCGGTGAAGTGAAATCAGTGGAATTAGTTGCTTTTTGGTGGTAACCA-AATCATTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1256 AGCAGGGGAAGGTATGATTATTACCGCTGGGGAATCGATTCACACACCCCACTTCCTTTC
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                                                                                                                                                                    564641 TGAAGTCCAGATTGAAGCTACTTTCCCCGATGGCACGAAACTTGTTACCGTGCATAATCC
                                                                                                                                                                                                                                                                                                                                                                                                               618 AATCCTTGC--ATGTGGGTAGCCATTTCCACTTCTTTGAAGCTAACAAGGCACTAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564102 TACCAATTTATGGGCAACCATTGAACAAGATTTATTGACCAAAGGTGATGAGTGTAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCGCGGGTAAAACTATCCGTGAGGGTATGGGTCAGAGCAATAGCCCTGATGAAAACAC
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                             CATC-GA-ACCAGATGAGCACTTCAAAGCGGGGAAGTGAAATTTGG--TTGCGATAAAG
                                                                                                                                                                                                                                                                                                                                                             564521 AGCCCACCCTACAAGGACAAAGATATGATCCCAGGCGAATACCAATTAGCCGAAGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAATTCAAGTTGGCTCGCATTACCATTTTTTGAAACCAATAATGCCCTTAAATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC-----TAGATTTAGTCATCACTAACGCGATGATTATCGA--CTACA-CCGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          563982 TCCGAATGTATTGGATTTTGTGATTACCAACGTGATGATCATTGATGCTAAATTAGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1196 CAAGGACATGCAAGATGGCGTAAGCCCTCATATGGTCGTGGGGTGTGGGCACAGAAGCACT
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                                                                                                                                                                                                                                                                                                                   ACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACTTGAGGTTACTAATGAAGGGCCTA

    CGCATTGGGGCAGGACAAACCCGCAAAGTGCAGTTGATTCCTCTTGGTGGCAGTAAAAA

                                                                                                                       CGATCTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCC
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                                                                                                                                                               Sequence I, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
TITLE OF INVENTION: The Heemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564998 TATATAAGGAGGATTTTTTTTTTTCAAGGGGCTTACAAAAATTCTGACAAAATATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <UNKNOWN>
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MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
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PRIOR APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE:
STREET: 9410 Key West Avenue
CITY: Rockville
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REGISTRATION NUMBER: 41,971
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TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
  2638 GAATCTTCATCAAA 2651
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Matches 1452; Conservative
                                               2721 GAÁACATCACGACA
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                                                                                                                                           US-09-557-884-1/c.
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564938 TCCTATTTTAGATTTTTACGTAAAATTCGCTGACTTTCGTATAATAAATTAAGGAATGA 564879
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Hamilton C Smith
J. Craig Vener
INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome,
Thereof, and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
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MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Fentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION - UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                562488 ATIGGGICAGCGATATITCCIATICTA 562462
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                                                                                                                    2576 TCTAGCCCAGCGCTACACTTTCTTCTA 2602
                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-643-990A-1/C
US-09-643-990A-1/C
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
Owen White
Owen White
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FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
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REGISTRATION NUMBER: 40,302
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SEQUENCE DESCRIPTION: SEQ ID NO:
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LENGTH: 1830121 base pairs
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STRANDEDNESS: double
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CATGITGCGCCAGCAGAAGAGTATICIAIGAAIGIGGGCTITITIGGGCAAAGGCAAIAG 1495
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                                                                                                                                                            CTCTAGCAAAAAACAACTTGTAGAACAAGTAGAAGCGGGCGCGATTGGTTTTAAATTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563262 ccccacrccrcccrrraccaaaacaccarrcarcarcarrracarracarracarracarrac
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b 564878 AAATATGCACTTAACTTCCAGAGAACAAGAAAACTGATGCTTTTCCTCGGGGGGAACT 564819	y 262 GGCTAGAAAGGGCAAAGGAGGGCTTAAAGCTCAACCAACC	y 322 TAGTGCCCATATTATGGACGAGCGCCGTGGAAAAAAAACCGTTGCCCGGCTTATGGA 381	382	y 442 CGATCTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCC 501			y 618 AATCCTTGCATGTGGGTAGCCATTTCACTTCTTTGAAGCTAACAAGGCACTAAAATT 675	y 676 CGATCGTGAAAAGCCTATGGCAAACGCCTAGATATTCCCTCTGGCAACACGCTA 730	y 731 -CGCATTGGGCAGGACAAACCCGCAAAGTGCAGTTGATTCCTCTTGGTGGCAGTAAAAA 789	y 790 agtgaftggcatgaacggcttgtgaataacatcgcggafgaacgccataaagc 849	y 850 GCTTGACAAGGCGAAATCTCACGGATTTATCAAGTAAGGAGACTCCCATGAAAATGAA 907	y 908 aaaacaagaatatgtaaatacctacgacccaccaaggcgataaagtgcgcttaggaga 967 	y 968 TACCGATCTTTGGGCAGAAGTAGAACATGACTATACCACCTATGGCGAAGAACTTAAATT 1027	y 1028 TGGCGGGGTAAAACTATCGTGAGGGTATGGGTCAGAGCAATAGCCCTGATGAAAACAC 1087	y 1088 CCTAGATTTAGTCATCACGCGATGATTATCGACTACA-CCGGGAT 1135 	y 1136 TTACAAAGCCGACATTGGGATTAAAACGGCAAAATCCATGGCATTGGCAAGGCAGGAAA 1195 	y 1196 caaggacatgcaagatggcgtaagccctcatatggtcgtggggtgtggggcacagaagcact 1255 	y 1256 agcagggaaggtatgattattaccgctggggaatcgattcacacaccacttcctttc 1315 b 563802 taacggtgcacatttaattgcaaccgctggtggtatcgatacccacattcactttatttg 563743
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2336 TCACGGCAAGGGAAATTTGACACCAGCATCACTTTTGTTTCCAAAGTCGCCTATGAAAA 2395
562728 ACAAGGCTTAGCAACAGCAACAGCAGTATTGTTTGTTTTCAAAGCCGCTGAAAAGC 562669 562729 563383 562789 563742 TCCACAACAAGCACAACATGCAATTGAAAGTGGCGTTACCACGTTAATTGGTGGTGGAAC 563683 563143 563083 563323 2095 TATGITTCAAGCGGCAGAAGCCTTGCCGGTAAACGTCGGATTTTTTGGTAAAGGCAACTG 563142 TGAAACCATTGCAGCAGAAGATATTTTGCATGATATGGGCGTCTTCTCCATTATGATTC TTCAACCCTAGATCCTCTGCGTGAGAAATTGAAGCGGGTGCATTAGGTTTAAAAATCCA TGAAGACTGGGGCACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAATA CGATTCTAACGCGTCTGTGCCCCACTCCCCAACCGGTTTATTACCGGCGAAATGTTTGGGCA cearccaarccricaarrccaacaccecacrerarrcraccerccaareraceerec CATGTTGCGCCAGCAGAAGAGTATTCTATGAATGTGGGCTTTTTGGGCAAAGGCAATAG CTCTAGCAAAAAACAACTTGTAGAACAAGTAGAAGCGGGCGCGATTGGTTTTAAATTGCA CGATGTGCAAGTTTGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATGACAC 1676 CCTAAATGCAATGAACGGGCGCCCATCCATGCCTACCACATTGAGGGAGCGGGTGGAGG ACACTCACCTGATGTTATCACCATGGCAGGCGAGCTCAATATTCTACCCTCCTCCACCAC TAAGAATAAAAAAGAATTTGGTAAGCTTCCTGAAGATGGCAAAGATAACGATAATTTCCG TAAGATGAAAATGCAACGTGGGTGAGCT----AGGTAATGAAGGAAACGATAACTTCCG CATTAAGCGCTACATCTCCAAATACACTATCAACCCCGCTTTGACCCACGGCGTGAGCGA GCATATTGGCTCGTTAGAAGTGGGTAAAATCGCAGATATCGTGTTATGGAAACCGATGTT TCCACAACAATTCCCTACCGCTCTAGCCAATGGCGTTACAACCATGTTTGGAGGCGGCAC AGGICCTGTAGATGGCACGAATGCGACTACTATCACTCCGGGCAAATGGAACTTGCACCG CCCCACTATTCCCTATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATG GTATATCGGCTCTGTGGAAGAGGGCCAAGATCGCCGACTTGGTGGTGTGGAATCCTGCCTT TTTTGGCGTAAAACCCAAAATCGTGATCAAAGGCGGTATGGTGGTCTTCTCTGAAATGGG CCACCACCTAGACAAACGCATCCGCGAGGATTTACAATTTTCTCAAAAGCCGTATCCGCCC 1916 CGGCTCTATCGCGCCTGAAGATGTGCTCCATGATATGGGTGTGATCGCGATGACAAGCTC GGATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTGCCGGA 1376 1616 1736 1856 2036 2096 2156 2216 2276 563622 1496 1556 1796 563022 562788 1316 1436 563562 1976 562908 ъ ą á ą ŏ a હ ည ≿ ည a g 25 25 ⋩ g ð ⋩ a ⋩

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NAME/KEY: misc feature
LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (51602)...(51602)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc feature
LOCATION: (107248)...(107248)
FEATURE:
FEATURE:
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LOCATION: (51786)...(51786)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (65309)...(65309)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                          NAME/KEY: misc feature
LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (45732)...(45732)
OTHER INFORMATION: n equals a,t,c,
FEATURE:
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (100091)...(100091)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals
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APPLICANT: Fleischmann et al.

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fraggistern No. 6846651

TITLE OF INVENTION: Thereof, and Uses Thereof

FILE REPERENCE: PB18662C1D1

CURRENT APPLICATION NUMBER: US/10/158,865

CURRENT RILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US 09/557,884

PRIOR APPLICATION NUMBER: US 08/476,102

PRIOR APPLICATION NUMBER: US 08/476,102

PRIOR APPLICATION NUMBER: US 08/426,787

PRIOR PILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1

SOOTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGRENT BARDISTER
                                                 562668 теататтсетеселадетгеесттйелелалаларды 562668 теататтестете
                                                                                                                                                 562608 ceraceraaaaakearcreerrearaareareraaceaceaacarracrerrearecrea 562549
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2396 TGGCGTGAAAAAGCTGGGCTTAGAGCGCCAAGTTCTACCGGTCAAAACTGCCGTAA 2455
                                                                                                                                                                                                     2516 AACCTTCGAGGTCTTTGTAGATGGCAAACTCTGCACCTCTAAACCCACCTCGCAAGTGCC 2575
                                                                                                  2456 CATCACCAAGAAAGACTTCAAGTTCAACGACAAAAACGGCAAAAATCACCGTCGATCCGAA 2515
                                                                                                                                                                                                                                                                                                                                          562488 ATTGGGTCAGCGATATTTCCTATTCTA 562462
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (4747)...(4747)
OCTHER INFORMATION: n equals a,t,c,
FEATURE:
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COCATION: (9921).
OTHER INFORMATION: n equals a,t,c,
FEATURE:
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,t,c,
FEATURE:
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10158865
Patent No. 6846651
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US-10-158-865-1/¢
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or ö ör or ᇅ 占 or or or ör ö ö ö or LOCATION: (152500)..(152500) OTHER INFORMATION: n equals a,t,c, or ö 5 ö NAME/KEY: misc feature LOCATION: (145171)..(145171) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (117136)...(117136) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (119924)..(119924) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (121344)...(121344) OTHER INFORMATION: n equals a,t,c, LOCATION: (122336)..(122336) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc_feature LOCATION: (139910)..(139910) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (140398)..(140398) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (142750)..(142750) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (145058)..(145058) OTHER INFORMATION: n equals a,t,c, LOCATION: (145942)..(145942) OTHER INFORMATION: n equals a,t,c, FEATURE:
NAME/KEY: misc_feature
LOCATION: (147197).. (147197)
OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (150841)..(150841) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (120038)..(120038) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (122167)...(122167) OTHER INFORMATION: n equals a,t,c, COCATION: (131340)..(131340) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc feature LOCATION: (131360)..(131360) JTHER INFORMATION: n equals a,t,c, NAME/KEY: misc_feature NAME/KEY: misc feature OCATION: (131340)..(13 NAME/KEY: misc feature NAME/KEY: misc_feature NAME/KEY: misc_feature

564938 TCCTATTTTAGATTTTTTACGTAAAATTCGCTGACTTTCGTATAATAAATTAAGGAATGA 564879 564461 TATTCTCGCTAATGTCGGCAGAAAAACCGTAAAATCGAAGTAACAAATTCAGGCGACCG 564402 564042 TGGTGGCGGTAAAAGCGTGCGTGATGGTATGGCTCAAAGCGGTACGGCAACTCGCGAAAA 563983 564998 TATATAAGGAGGATTTTTTTTTTTCAAGGGCTTACAAAAAATTCTGACAAAATATTTT 564939 564701 ATATGGGGGAACACTTTTAACCGTTGATGATGTCATGGAAGGTGTGGGGGAAATGGTTCA 564642 564581 AATCAGATAACCGWAGGGTGGGCTTTAGCCCACAAAATAAAAATATCAATGGTGGGCTAA 564522 564521 AGCCCACCCTACAAGGAACAAAGATATGATCCCAGGCGAATACCAATTAGCCGAAGGCGA 564462 564401 CCCAATTCAAGTTGGCTCGCATTACCATTTTTTTGAAACCAATAATGCCCTTAAATTTGA 564342 1028 TGGCGCGCGTAAAACTATCCGTGAGGGTATGGGTCAGAGCAATAGCCCTGATGAAAACAC 1087 322 TAGTGCCCATATTATGGACGAGGCGCCGTGGAAAAAAAACCGTTGCCCAGCTTATGGA 381 850 GCTTGACAAGGCGAAATCTCACGGATTTATCAAGTAAGG--AGACTCCCATGAAAATGAA 564878 AAATATGCACTTAACTTCCAGAGAACAAGAAAACTGATGCTTTTCCTCGCGGGCGAACT 564641 TGAAGTCCAGATTGAAGCTACTTTCCCCGATGGCACGAAACTTGTTACCGTGCATAATCC 502 CATC-GA-ACCAGATGAGCACTTCAAAGCGGGGGAAGTGAAATTTGG--TTGCGATAAAG 618 AATCCTTGC--ATGTGGGTAGCCATTTCCACTTCTTTGAAGCTAACAAGGCACTAAAATT 564281 ACCCGGTGAAGTGAAATCAGTGGAATTAGTTGCTTTTGGTGGTAACCA-AATCATTTATG 564222 GTTTCCATAATCAATTGATGGCAATTATAAGGTAGGCAAGATGGCATTAACAATTTC 968 TACCGATCTTTGGGCAGAAGTAGAACATGACTATACCACCTATGGCGAAGAACTTAAATT 143 AAAAAGTAACGAAATTAGGACTATAATCCCATTGCCTTTAAAATTTAACACAAGGAGT-A 564758 recraercarriacaagaeecaecaagaagaaagaa---reagreragegaagreareca 731 - CGCATTGGGGCAGGACAAACCCGCAAAGTGCAGTTGATTCCTCTTGGTGGCAGTAAAAA 564341 CCGCACTTTGGCACGTGGAATGCGCTTAAATGTTCCATCTGGCAATGCGGTGCGTTTTGA 790 AGTGATTGGCATGAACGGGCTTGTGAATAACATCGCGGATGAACGCCATAAACATAAAGC 908 AAAACAAGAATATGTAAATACCTACGGACCCACCAAAGGCGATAAAGTGCGCTTAGGAGA 564102 TACCAATTTATGGGCAACCATTGAACAAGATTTATTGACCAAAGGTGATGAGTGTAAATT CGATCGTGAAAAAGCCT---ATGGCAAACGCCTAGATATTCCCTCTGGCAACACGCTA--202 ATAGGTGAAACTCACACCCAAAGAGCAAGAAAAGTTCTTGTTATATTATGCGGGCGAAGT 442 CGATCTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCC 558 ACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACTTGAGGTTACTAATGAAGGGCCTA Gaps Length 1830121; 37; Indels Score 665.4; DB 3; Pred. No. 5.9e-154; 1; Mismatches 1057; Query Match
23.1%;
Best Local Similarity 57.0%;
Matches 1452; Conservative 1 919 g 셤 g g 셤 셤 원 셤 a Š 셤 ઠે g 8 ઠ 셤 ઠ ઠ 셤 δ ઠ 임 ઠ 셤 ð ద ઠે ઠે ઠે ઠ à

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562548 ACGTTATGAAGTTCGAGTGGAGGGAGTTAATTACCTGTGAACCAGTGGATAGCGTACC 562489
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                                                                                                                                     CGATTCTAACGCGTCTGTGCCCACTCCCCAACCGGTTTATTACCGCGAAATGTTTGGGCA
                                                                                                                                                                      62788 CGÁTCCAÁATGCCTCAATTCCAACACCGCAACCTGTATTCTACCGTCCAATGTACGGTGC
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Pred. No. 4.4e-151;
0; Mismatches 633;
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Patent No. 6605709
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Best Local Similarity 62.2%;
Matches 1052; Conservative
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; ORGANISM: Proteus mirabilis
US-09-543-681A-1857
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US-09-543-681A-1857
                                                          2216
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                     563982 ICCGAATGTATTGGATTTTGTGATTACCAACGTGATGATCATTGATGCTAAATTAGGCAT 563923
                                                                                                             563922 TATCAAAGCCGATATTGGTATTCGTGATGGGCGTATTGTGGGTATTGGACAAGCAGGTAA 563863
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                                                                                                                                                                                                                             1256 AGCAGGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACCCCACTTCCTTTC 1315
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CC-----TAGATTTAGTCATCACTAACGCGATGATTATCGA--CTACA-CCGGGAT 1135
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                                                                                                                                                                                                                                                                                                                                 TGAAGACTGGGGCACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAATGAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                         563682 TGGCCCTGCTGATGGTACACACGCAACCACTTGTACCCCTGGCGCATGGTATATGGAACG
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                                                                          TTACAAAGCCGACATTGGGATTAAAAACGGCAAAATCCATGGCATTGGCAAGGCAGGAAA
                                                                                                                                                     CAAGGACATGCAAGATGGCGTAAGCCCTCATATGGTCGTGGGGTGTGGGCCACAGAAGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGATGTGCAAGTTTGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATGACAC
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GENERAL INFORMATION:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL:)
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERRINGS: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1857 1031 1091 7 1152 GGGATTAAAAACGGCAAAATCCATGGCATTGGCAAGGCAGGAAACAAGACATGCAAGAT 1211 84 GATCTTTGGGCAGAAGTAGAACATGACTATACCACCTATGGCGAAGAACTTTAAATTTTGGC GCGGGTAAAACTATCCGTGAGGGTATGGGTCAGAGCAATAGCCCTGATGAAAACACCCTA CAAGAATATGTAAATACCTACGGACCCACCAAAGGCGATAAAGTGCGCTTAGGAGATACC caagerrargeegararerrregeeceaacaacaagegegareerrregegarrageaarace GAGCTGTTTCTTGAAATTGAAAAGATTTCACCACTTATGGCGAAGAGGGTCAAATTTGGT GGTGGTAAAGTTATTCGTGATGGTATGGGCCAAAGCCAAGTTGTTAGTGCTGAGTGTGT GATGITCIGATCACCAATGCCATTATTTAGATTATTGGGGCCATTGTAAAAGCAGATATT GATTIAGICATCACTAACGCGATGATTATCGACTACACCGGGGATTTACAAAGCCGACATT Gaps 9 Length

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1339 GCACTTATCATAAAAGGTGGTATGGTCGCTTATGCGCCAATGGGGGATATTAATGCGGCT 1398
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Fatent No. 5783436
GENERAL INFORMATION:
APPLICANT: Robert P. Hausinger
TITLE OF INVENTION: Mutant Urease and Method
TITLE OF INVENTION: of Use Por Determination
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
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ZIP: 4864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: Brorage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,513
FILING DATE: 11-NOV-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/687,645
FILING DATE: July 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeed
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-309
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFO
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STRANDENNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: CDNA
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CITY: Okemos
STATE: Michiga
COUNTRY: USA
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                                                                                                                                  321 -GCCCAA-TGTGGATATTGTCATTGGCCCCGGAACAGAAGTTGTTGCGGGAGAAGGTAAA 378
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                     265 GGCATTAAAGATGGCCGTATTGTCGGTATTGGCAAGGCAGGTAATCCAGATGTTCA--
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APPLICANT: RODert P. Hausinger TITLE OF INVENTION: Mutant Ureast TITLE OF INVENTION: of Use For DE TITLE OF INVENTION:
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Modification at position 1312
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NAME/KEY: CDNA encoding mutant ux
NAME/KEY: 'H2190
LOCATION: Modification at positic
LOCATION: glutamine
IDENTIFICATION METHOD: Sequencing
OTHER INFORMATION:
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                  ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Klebsiella au
STRAIN: CG253
INDIVIDUAL ISOLATE:
CELL TYPE: N/A
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Matches 1048; Conservative
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       1123 ACTACACCGGGATTTACAAAGCCGACATTGGGATTAAAAACGGCAAAATCCATGGCATTG
                                                                        885 ATCACTGGGGGATCGTTAAGGCCGGTATCGGCGTGAAGGACGGCCGGATCTTCGCCATCG
                                                                                                                                         GCAAGGCAGGAAACAAGGACATGCAAGATGGCGTAAGCCCTCATATGGTCGTGGGTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ဌ
                                                                                                                                                                                                                                    CIPEL 4864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,645B
FILING DATE: July 26, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTING DATE:
ATTING DATE:
ATTING DATE:
ATTING DATE:
APPLICATION NUMBER:
FILING DATE:
ARGASTRATION NUMBER:
REGISTRATION NUMBER:
REGISTRATION NUMBER: MSU 4.1-309
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Modification at position 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEFONDE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5846752e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH. A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing
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NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: glutamine
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 1048; Conservative
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STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
                                                                                                 STREET: 2190 COM
CITY: Okemos
STATE: Michigan
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2400
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LOCATION:
LOCATION:
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1500 AGCAAAAAACAACTIGIAGAACAAGIAGAAGCGGGCGCGATIGGITITIAAATIGCAIGAA 1559
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310 GATATCCAGCCCAACGTCACC----ATCCCCATCGGTGCCTCGACGGAAGTGATTGCC 363
                                                                                                                                                                                                                              1260 GGGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACACCCCACTTCCTTTCTCCA
                                                                                                                                         364 GCCGAAGGAAAATTGTCACCGCCGGGATCGATACCCATATTCACTGGATCTCG
                                                                                                                                                                                                                                                                                                                                                               484 CCGGCCGCGGCACCCATGCCACCTGCACCCCGGGCCCGTGGTATATCTCACGCATG
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                                                                                                                                                                                               CAACAATTCCCTACCGCTCTAGCCAATGGCGTTACAACCATGTTTGGAGGCGGCACAGGT
                                                                                                                                                                                                                                                                                                           1380 CCTGTAGATGGCACGAATGCGACTACTATCACTCCGGGCAAATGGAAACTTGCACCGCATG
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TILLE OF INVENTION: PROMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION UNDER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                  2079 CGATGTTTGGCGCGCTGGGCAGCGCCCGCCATCACTGCCGCCTCACCTTCCTGTCGCAGG 2138
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                               1959 GGTCACCAGCCTTCTTCGGCGTGAAACCGGCCACCGTGATCAAAGGCGGCATGATCGCCA 2018
                                                                                                                                         2019 TCGCGCCGATGGGCGATATCAATGCCTCTATTCCGACCCCGCAGCCGGTGCACTACCGCC 2078
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                                                                                  2263 TCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCACTCCCCAACCGGTTTATTACCGCG
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2.09-489-019A-2045
; Sequence 2045, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
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ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 60.8%;
Matches 1028; Conservative
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                        1384 ATCAATGCCTCTATTCCGACCCCGCAGCCGGTGCACTACCGCCCGATGTTTGGCGCGCTG 1443
                                            2400 GTGAAAGAAAAGCTGGGCTTAGAGCGCCAAGTTCTACCGGTCAAAAACTGCCGTAAACTG
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Search completed: August 10, 2006, 02:19:22 Job time : 542 secs

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61 ACTIGITAATRCTAFITAATTTTTTAATAATTACTTAFTATCATATATAATAATTA
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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Sequence 10, Appli
Sequence 7, Appli
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Sequence 2847, A
Sequence 11, Appli
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                                                                                                           (without alignments)
7598.724 Million cell updates/sec
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                                                                                         August 10, 2006, 01:39:48 ; Search time 4662 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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3 US-09-904-994B-4

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3 US-09-904-994B-1

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10 US-10-35-977-3849-9

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10 US-10-500-447A-5-9

10 US-10-10-10-11

10 US-10-10-10-11

11 US-10-10-10-11

12 US-10-11-11
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Maximum Match 100%
Listing first 45 summaries
                                                              - nucleic search, using sw model
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Match Length DB
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Sequence 33102, A Sequence 32560, A Sequence 32560, A Sequence 23823, A Sequence 23823, A Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 11659, A Sequence 14654, A Sequence 22, Appl Sequence 226, Appl Sequence 256, Appl Sequence 266, A Sequence 217, Appl Sequence 2154, Appl Sequence 21554, Appl 
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US-10-282-122A-33102

US-10-282-122A-33950

US-10-282-122A-34990

US-10-282-125A-680

US-10-282-122A-2026

US-10-282-122A-2026

US-10-282-122A-13582

US-10-282-122A-1454

US-10-282-122A-1454

US-10-282-122A-1454

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US-10-282-122A-2069

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US-10-282-122A-14888
US-09-738-626-1
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| Publication No. US20040005325A1
| GENERAL INPORMATION:
| APPLICANT: AKZO No. US2004000525A1el N.V.
| TITLE OF INVENTION: Helicobacter vaccine PILE REFERENCE: Degedesequenties
| CURRENT APPLICATION NUMBER: US/09/904,994B
| CURRENT FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 21
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 1
| LENGTH: 2883
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Matches 2883; Conservative
                                                    ; NAME/KEY: CDS
; LOCATION: (897)..(2603)
US-09-904-994B-1
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ND 61 CCAAAGAGCAAGAAAAGTTCTTGTTATATGCGGGGGAAGTGGCTAGAAAGCGCAAAG 120	179 CAGAGGGTTAAAGCTCAACCGAAGCCATTGCTTACATTAGTGCCCATATTATGG 338		y 399 TGAAAAAAGTAATGCCCGGGTGGGTAATATGTTCCCGATCTAGGTGTAGAAG 458	y 459 CCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCCCATCGAACCAGATGGC 518	y 519 ACTTCAAAGCGGGGGGAATTTGGTTGCGATAAAGACATCGAGGCTCAATGCAGGCA 578	y 579 AAGAAGTAACCGAACTTGAGGTTACTAATGAAGGCCTAAATCCTTGCATGTGGGTAGCC 638	y 639 ATTTCCACTTCTTGAAGCTAAAAGGGACTAAAATTCGATCGTGAAAAAGCCTATGGCA 698	y 699 AACGCCTAGATATTCCCTCTGGCAACACGCTTGGGGCAGGACAAAAAG 758 	y 759 IGCAGTIGATICCTCTIGGIGGCAGTAAAAAGTGATIGGCATGAACGGGCTTGIGAATA 818 	y 819 acatggggatgaaggccataaacataaagggcttgacaaggggaaatctcaggattta 878 	y 879 TCAAGTAAGGAGTCCCATGAAAATGAAAAACAAGAATATGTAAATACCTACGGACCC 938 	y 939 ACCAAAGGGGATAAAGTGCGCTTAGGAGATACCGATCTTTGGGCAGAAGTAGAACATGAC 998	y 999 TATACCACCTATGGCGAAGAACTTAAATTTGGCGGGGTAAAACTATCCGTGAGGGTATG 1058 	y 1059 GGTCAGAGCAATAGCCCTGATGAAAACACCCTAGATTTAGTCATCATCATAACGCGATGATT 1118	y 1119 arcgactacaccgggatttacaaagccgacattgggattaaaaacggcaaaatccatggc 1178 	y 1179 attggcaaggaaacaaggacatgcaagatggcgtaagccctcatatggcgt 1238 	y 1239 GTGGGCACAGAAGCACTAGCAGGAAGGTATGATTACTGCTGGGGGAATCGATTCA 1298 	y 1299 CACACCACTTCCTTCTCCACAATTCCCTACCGCTCTAGCCAATGGCGTTACAACC 1358
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	1539 ATTGGTTTTAAATTGCATGAAGACTGGGGCACCAACTGCGATCGAT	1899 CAAAGCCGTATCCGGCTCTATCGCGGCTGAAGATGTGCTCCATGATATGGGTGTG 1958	2019 ACITICALMANTO CONTRACTOR CANDANGAMINE CONTRACTOR C	2139 ACCCACGGCGAGAGTATATCGGCTCTGTGGAAGAGGCAAGATCGCCGACTTGGTG 2198	2259 GTCTTCTCTGAAATGGGCGATTCTAACGGGTCTGTGCCCCACTCCCCAACGGGTTTATTAC 2318 [

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LENGTH: 2407
TYPE: DNA
ORGANISM: Helicobacter felis
                                                                                                                               Query Match
Best Local Similarity 93.6'
Matches 2251; Conservative
                                                                                ; NAME/KEY: CDS
; LOCATION: (693)..(2399)
US-09-904-994B-10.
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NAME/KEY: CDS
LOCATION: (2)..(682)
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Best Local Similarity 93.3%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 145;
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Publication No. US2004006325A1
GENERAL INFORMATION:
APPLICAMT: AKZO No. US20040005325A1e1 N.V.
TITLE OF INVENTION: Helicobacter vaccine
FILE REFERENCE: Degoedsequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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; LOCATION: (694)..(2181)
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TYPE: DNA
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Sequence 1, Application US/10639273
Publication No. US20040142343A1
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Zhu, Jiaqian

US-10-639-273-1

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TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS FILE REFERENCE: 19603/381 10639,273
CURRENT APPLICATION NUMBER: US/10/639,273
CURRENT FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: 60/404,337
PRIOR FILING DATE: 2003-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTING VET: 2.1
LENGTHARE: PATENTING VET: 2.1
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TYPE: DNA ORGANISM: Helicobacter bizzozeronii
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                                                          3159 AACATGACTGCACCACTTATGGCGAAGAATTAAGTTTGGTGGCGGTAAAACCATTCGCG 3218
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Sequence 4, Application US/10639273
Sequence 4, Application US/10639273
FUBLICATION NO. US20040142343A1
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
FILE REPERENCE: 19603/3881
CURRENT APPLICATION NUMBER: US/10/639,273
CURRENT APPLICATION NUMBER: 60/404,337
PRIOR PILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: 60/404,337
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1 2370 ö TTAGGAGATACCGATCTTTGGGCAGAAGTAGAACATGACTATACCACCTATGGCGAAGAA 1019 900 AAAATGAAAAAACAAGAATATGTAAATACCTACGGACCCACCAAAGGCGATAAAGTGCGC 959 99 4239 AAAAAGGCGATAATGACAACTTCCGCATCAAGCGCTACATTTCCAAATACACCATCAACC 2071 ATGGCAAAGATAACGATAATTTCCGCATTAAGCGCTACATCTCCAAATACACTATCAACC CCGCTTTGACCCCACGGCGTGAGCGAGTATATCGGCTCTGTGGAAGAGGGCAAGATCGCCG 4359 ATTIGGIGCTTIGGAGICCTGCGTTCTTIGGCATTAAACCCAACAIGATCAICAAAGGCG GTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCCACTCCCCAACCGG 4539 TTGTATCCCAAGTGGCTTATGACAACGGCATTAAAGAAGAAGTTGGGCTTGCAAGGAGTGG 4299 ccecratrecacacecarrrcreaararercecrereragaagreegecaaarrcecee 2191 ACTTGGTGGTGTGGAATCCTGCCTTTTTTGGCGTAAAACCCAAAATCGTGATCAAAGGCG TITATITACCGCGAAATGITIGGGCATCACGGCAAGGCGAAAITIGACACCAGCATCACTT TTGTTTCCAAAGTCGCCTATGAAAATGGCGTGAAAGAAAAAGCTGGGCTTAGAGCGCCAAG 4599 TTTTGCCAGTTAAAACTGCCGCAACATCACCAAAAAAGACCTCAAATTCAACGATGTTA CGGCAAAAATCACCGTCGATCCGAAAACCTTCGAGGTCTTTGTAGATGGCAAACTCTGCA 4659 CCGCACACATCGAAGTCATCCTGAAACCTACAAAGTTAAAGTGGATGGCAAAGAGGTTA Gaps crrccaaagcagcggaraaaarcagccragcacaacrcracaacrrgrrgrrcragg 4772 CCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTAGG °; Length 1710; Indels 32.7%; Score 940.8; DB 8; 72.0%; Pred. No. 3e-196; iive 0; Mismatches 477;

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	RESULT 8 US-10-476-313-10 Sequence 10, Application US/10476313 Publication No. USC0040241175A1 SEQUENCE 10, Application US/10476313 Publication No. USC0040241175A1 SEQUENCE INVESTIONS: ABEREX APPLICANT: BOYLE, USFPERSY APPLICANT: BOYLE, USFPERSY APPLICANT: BOYLE, USFPERSY TILES DEPRENCE: BDMP-002 CURRENT FILING DATE: 2003-10-24 PRIOR FILING DATE: 2001-05-25 PRIOR PILING DATE: 2001-05-25 PRIOR APPLICATION NUMBER: PF541 PRIOR PILING DATE: 2001-05-25 PRIOR
1020 CTTAAATTTGGCGGGGTAAAACTATCCGTGAGGGTATGGGTCAGAGCAACCAGT	1560 GACTGGGGCACAACACCAAGTGCATCACTCTCAGGCGTGCAATGAATACGAT 726 [1610] [

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APPLICANT: Kleanthous, Harold
APPLICANT: Kleanthous, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean Francois
APPLICANT: Tomb, Jean Francois
APPLICANT: Ownen, Raymond P.
APPLICANT: Ownen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome
                                                                    1800 ACTATTCCCTATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGCCAC 1859
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1447 GGTAAAGCTAAATACGATGCAAACATCACTTTTGTGTCTCAAGCGGCTTATGACAAAGGC
                           847 GCTCCTGACATTATTAAAGTGGCCGGTGAACACAACATCCTACCCGCTTCCACTAACCCC
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                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1710
SEQUENCE DESCRIPTION: SEQ ID NO: 3849:
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
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                                                                                                                                 FEATURE
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                       897 GCTCCTGATATTATAAAGTAGCTGGTGAACACAACATTCTTCCCGCTTCCACTAACCC
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Amudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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FILE REFERENCE: 06132/043002; CURRENT APPLICATION NUMBER: US/09/895,913A; CURRENT FILING DATE: 2001-06-29; PRIOR APPLICATION NUMBER: US 08/881,227; PRIOR FILING DATE: 1997-06-24; NUMBER OF SEQ ID NOS: 368; SOFTWARE: PSEÇEQ for Windows Version 4.0; SEQ ID NO 251; LENGTH: 1815
                                                                                                                                                                           TYPE: DNA
ORGANISM: Helicobacter pylori
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Best Local Similarity 70.0
Matches 1193; Conservative
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                                                                     427 CAACAAATCCCTACAGCTTTTGCAAGCGGTGTAACAACCATGATTGGTGGCGGAACTGGT
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APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Tavakic, Judith
APPLICANT: Tavakic, John
APPLICANT: Travic, R.
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Wi, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: 60/191, 078
FRIOR APPLICATION NUMBER: 60/202, 20
FRIOR APPLICATION NUMBER: 60/207, 727
FRIOR PILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-12-09
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70.0%;
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CCTGCTGATGGCACTAACGCAACCACTATCACTCCAGGTAGAAGAAATTTAAAATGGATG
                                                                1440 TIGCGCGCAGCAGAAGAGTATICTATGAATGTGGGCTTTTTGGGCAAAGGCAATAGCTCT
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                                                                                                  547 CTCAGAGCGCAGAAGAATATTCTATGAACTTAAGTTTCTTAGCTAAAGGTAACGCTTCT
                                                                                                                                                                                          607 AACGATGCAAGCTTAGCCGATCAAATTGAAGCCGGTGCGATTGGCTTTAAAATCCACGAA
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                                                                                                    1567 ACTAPAPAPAGACATGCAATTCAACGACACTACCGCTCACATTGAAGTCAATCCTGAAACT 1626
                                                                                                                                                                                   TACCATGTGTTCGTGGATGGCAAAGAAGTAACTTCTAAACCAGCCAATAAAGTGAGCTTG 1686
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Sequence 5. Application US/10500447A
Publication No US20050150016A1
GENERAL INFORMATION:
APPLICAMT: PARK, Hee-Sung
TITLE OF INVENTION: Method for producing a recombinant protein using pollen
FILE REFREENCE: VID0940518US/PCT
CURRENT APPLICATION NUMBER: US/10/500,447A
CURRENT FILING DATE: 2004-06-30
PRIOR PILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
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ORGANISM: Helicobacter pylori
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Best Local Similarity 69.8%;
Matches 1189; Conservative
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                                                                             ACTAAAAAAAGCATGCAATTCAACGACACTACCGCTCACATTGAAGTCAATCCTGAAACT 1626
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Pred. No. 3.8e-182;
0; Mismatches 517;
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT MCKENZIE, BRENT
APPLICANT BOYLE, UBFPEREY
APPLICANT LEW, ANDREW
APPLICANT LEW, ANDREW
TILLE OF INVENTION: Antigen Targeting
FILE REFERENCE: BDW-002
CURRENT APPLICATION NUMBER: US/10/476,313
CURRENT FILING DATE: 2003-10-24
PRIOR APPLICATION NUMBER: PR5241
PRIOR APPLICATION NUMBER: PR5241
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VEYSION 3.1
                                                                                                                                                                1687 GCACAACTCTTTAGCATTTTCTAG 1710
                                                                                                                                        GCCCAGCGCTACACTTTCTTCTAG 2603
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Best Local Similarity 69.7%;
Matches 1187; Conservative
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ORGANISM: Helicobacter pylori
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a, t, g or
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OTHER INFORMATION: n equals a, t, g
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NAME/KEY: misc_feature
LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a,
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LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals a,
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals a,
                                                                                                                                           LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a,
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LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals a,
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a,
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals a,
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LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals a,
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals a,
FEATURE:
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LOCATION: (102596)...(102696)
OTHER INFORMATION: n equals a,
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a,
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals
                                    NAME/KEY: misc feature
LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals
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LOCATION: (55369)..(55
                                                                                                                                                                                                                                                     Sequence 1, Application US/10329670;
Sequence 1, Application US/10329670;
Publication No. US20040018503A1
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragritte OF INVENTION: Thereof, and Uses Thereof
FILE REPRENCE: PB18671
CURRENT APPLICATION NUMBER: US/10/329,670
CURRENT APPLICATION NUMBER: US 09/643,990
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1830121
1507 ATTAAAGAAGAATTAGGGCTTGAAAGACAAGTGTTGCCGGTAAAAATTGCAGAAATATC 1566
                                        2460 ACCAAGAAAGACTTCAAGTTCAACGACAAAACGGCAAAAATCACCGTCGATCCGAAAAACC 2519
                                                                1567 ACTAAAAAAGACATGCAATTCAACGACACTACGCTCACATTGAAGTCAATTCTGAAACT 1626
                                                                                                                                              1627 TACCATGTGTTCGTGGATGCCAAA-GAAGTAACTCTAAACCAGCCAATAAAGTG 1679
                                                                                                                        2520 TTCGAGGTCTTTGTAGATGGCAAACTCTGCACCTCTAAACCCACCTCGCAAGTG 2573
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LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals a, t, g or
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ORGANISM: Haemophilus influenzae
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a,
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LOCATION: (9921)
OTHER INFORMATION: n equals a,
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LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals a,
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a,
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (44905)..(44905)
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US-10-329-670-1/c
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LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals a,
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a,
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LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a,
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LOCATION: (131360)..(131360)
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LOCATION: (139910)..(139910)
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LOCATION: (140398)..(140398)
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a,
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LOCATION: (145<u>9</u>42)..(145942)
OTHER INFORMATION: n equals a,
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals a,
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a,
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LOCATION: (145171)...(145171)
OTHER INFORMATION: n equals a,
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LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (152530)..(152530)
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564938 TCCTATTTTAGATTTTTACGTAAATTCGCTGACTTTCGTATAATAAATTAAGGAATGA 564879
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143 AAAAAGTAACGAAATTAGGACTATAATCCCATTGCCTTTAAAATTTAACACAAGGAGT-A
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22790, A
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Sequence 11112, A
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US-11-348-413-11113

US-11-348-413-11115

US-10-471-571A-3255

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8 US-11-266-748A-313484 6 US-10-517-441-683 6 US-10-249-902-14592 6 US-10-517-441-698 6 US-10-517-441-424 6 US-10-517-441-424 6 US-10-517-441-426 6 US-10-517-441-409 8 US-11-26-748-61353 8 US-11-26-748-61353 6 US-10-517-441-919 6 US-10-517-441-919 6 US-10-517-441-565 8 US-11-216-545-1530 8 US-11-216-545-1530 8 US-11-216-549-902-21317 8 US-11-218-902-21517 8 US-11-218-902-21517 8 US-11-218-903-21517 8 US-11-218-903-21517 8 US-11-218-903-21517 8 US-11-218-903-21517 8 US-11-218-903-21517	ALIGNMENTS	1837 cus Saprophyticus Nu 11/021,837 23 9/533534 9/600680 phyticus Score 615, DB 9; Pred. No. 8.7e-135; 0; Mismatches 1025; 17	AGCCATTGCTTACATTAGTGCCCATATTATGGACGAGGGCGCCGTGGAAAAAACCG
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1249 AAGCACTAGCAGGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACACCCACT 1306	1309 TCCTTTCTCCACAACAATTCCCTACGGTTCTAGCCAATGGGGTTACAACCATGTTTGGAG 1366	1369 GCGGCACAGGTCCTGTAGATGCCACGATGCGACTACTATCACTCCGGGCAAATGGAACT 1:426	1429 TGCACCGCATGTTGCGCGCAGCAGAAGAGTATTCTATGAATGTGGGCTTTTTGGGCAAAG 1486		1549 AATTGCATGAAGACTGGGGCACAACACCAAGTGCGATCGAT	1609 ATGAATACGATGTGCAAGTTTGTATCCACGCGATACAGTCAATGAGGCAGGTTATGTAG 1668 122 ATGAGTTTGATRTTCAAGTCGCTTTACATGCAGAXACATTAAATGAAGCTGGATTTATGG 781	1669 ATGACACCCTAAATGCGATGAACGGGCGCCATCCATGCCTACCACATTGAGGGAGG	1729 GIGGAGGACACTCACCTGAIGTIAICACCAIGGCAGGGGGGGGGG	1789 CCACCACCCCCATTTCCCTATACCATTAATACGGTTGCAGAACACTTAGACATGCTCA 1848	1849 TGACATGCCACCTAGACAAACGCATCCGCGAGGATTTACAATTTTCTCAAAGCCGTA 1908 	1909 TCCGCCCCGGCTCTATCGCGGCTGAAGATGTCCTCCATGATATGGGTGTGATCGCGATGA 1968 1022 TACGTAAGGAAACTATAGCAGCAGAAGAYGTATTACAAGATATGGGCGTATTAGTATGG	1969 CAAGCTCGGATTCGCAAGCAATGGGGCGTGCAGCGAAGTGATTCCTCGAACTTGGCAGA 2028	2029 CTGCGGATAAGAATAAAAAGAATTTGGTAAGCTTCCTGAAGATGGCAAAGATAACGATA 2088 1142 TTGCACACCGTATGAAAGAACAACGCGGACCAYTAGATGGTGACTTTGAATATCACGATA 1201	2089 ATTTCGCATTAAGGGTACATCTCCAAATACACTATCAACCCCGCTTTGACCCACGGG 2148	2149 TGAGGGGTATATCGGCTCTGTGGAAGAGGGCAAGATCGCCGACTTGGTGGTGTGGAATC 2208	2209 CIGCCTTTTTGGCGTAAAACCCAAAATCGTGATCAAAGGCGGTATGGTGGTCTTCTCTG 2268	2269 AAATGGGGATTCTAACGCGTCTGTCCCCAACCGGTTTATTACCGCGAAATGT 2328	
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                                                                                                                                                GCCGTAACATCACCAAGAAAGACTTCAAGTTCAACGACAAAACGGCAAAAATCACCGTCG 2508
                                                                                                                                                                                                                                                                                      TTAGAAATTTAACTAAGGCAGATATGAAAATAATAATGCTACACCTAAAATAGATGTAG 1621
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                                                                                                  ATGAAAATGGCGTGAAAGAAAGCTGGGCTTAGAGCGCCCAAGTTCTACCGGTCAAAACT
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Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
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SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 3299
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<pre>g, or t Score 528.6; DB 8; Length 2673; Pred: No. 7.7e-115;); Mismatches 729; Indels 3; Gaps 1;</pre>	6 6 6 6 6	1868 CAAACGCATCCGCGAGGATITACAATITTCTCAAAGCCGTATCGCCCCGGCTCTATCGC
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    GCGTAAGCCCTCATATGGTCGTGGGTGTGGGCACAGAAGCACTAGCAGGGGAAGGTATGA
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                                                                                                                                                                                GTAACATCACCAAGAAAGACTTCAAGTTCAACGACAAAAACGGCAAAAATCACCGTCGATC 2511
                                                                                                                                                                                                                                                                          CGAAAACCTTCGAGGTCTTTGTAGATGGCAAACTCTGCACCTCTAAACCCCACCTCGCAAG 2571
                                                                                                                                                                                                                                                                                                                       CTGAAACCTACACGCTTACTGCTGATGGAGGGTTTTTGAGATGTCAACCAAACACCCACAG 2528
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GGCATCACGGCAAGGCGAAATTTGACACCAGCATCACTTTTGTTTCCAAAGTCGCCTATG
                                            GTGCATTTGGAGGGGCTGGAAGTGCCAACTCTATAGCATTTGTGAGCAAGGCTGCTAAAG
                                                                                           AAAATGGCGTGAAAGAAAAGCTGGGCTTAGAGCGCCCAAGTTCTACCGGTCAAAAACTGCC
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APPLICANT: McLaird, Paul L.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
TITLE OF INVENTION: Corn.
FILE REFERENCE: 38-21 (53660)8
CURRENT APPLICATION NUMBER: US 60/606,880
PRIOR PAPLICATION NUMBER: US 60/606,880
PRIOR FILING DATE: 2005-09-01
PRIOR FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 25043
SOFTWARE: Patentin version 3.2
SEQ ID NO 14860
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                                                                                                                                                                                                                                                                                                                                                                   TGCCTCTAGCCCAGCGCTACACTTTCTTCTAGGCA 2606
                                                                                                                                                                                                                                                                                                                                                                                                2529 TACCACTATCTCGGAATTACTTCCTCTTTTAGACA 2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14860, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
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LOCATION: (16)...(16)
OTHER INFORMATION: n is a, c, g, or
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                                                                                                            AcAGCAGGTCGAGAAGCCTCGCCTCCGAGTCACGACTCTTCTCGGTGGCGCGCCCCGG 3115
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                       2996 ATGTGAAGGAAAATTGTCACTGCAGGAATTGACACACGCCATTTTATATATGCCC 3055
                                                                                                                                                                                                    TCCAACTGAGGGATCAAATGCGACTACATGCACACCGGCTCCAAATCAGTTCAAGACGAT 3175
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US-11-348-413-11113/c

Sequence 11113, Application US/11348413

; Publication No. US20060160121A1

; GENERAL INFORMATION:
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APPLICANT: CHEN, Xia
APPLICANT: SESHAN, Kalpathi R.
APPLICANT: SESHAN, Kalpathi R.
APPLICANT: WUG, Chiung-Yu
APPLICANT: WUG, Jianh-Juen
TITLE OF INVENTION: Attenuated Vaccine Useful for
TITLE OF INVENTION: Immunizations Against Coccidioides spp. Infections
FILE REFERENCE: 5.9552000600
CURRENT APPLICATION NUMBER: US 60/633,399
PRIOR APPLICATION NUMBER: US 60/633,399
PRIOR APPLICATION NUMBER: US 60/633,399
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 4.0
                         GCGTGAAAGAAAAGCTGGGCTTAGAGCGCCAAGTTCTACCGGTCAAAAACTGCCGTAACA
                                                                                                          TCACCAAGAAAGACTTCAAGTTCAACGACAAAACGGCAAAAATCACCGTCGATCCGAAAA
                                                                GTGTCGCAACGGAGTACAGACTAGAAAAGAGGTGGAAGCTGTAGGCCGTGTTCGAGGCC
                                                                                                                                                                                                    CCTTCGAGGTCTTTGTAGATGGCAAACTCTGCACCTCTAAACCCCACCTCGCAAGTGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 36, Application US/11292431; Publication No. US20060121061A1; GENERAL INFORMATION:
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ORGANISM: Coccidioides posadasii
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APPLICANT: CHEN, Xia
APPLICANT: SESHAN, Kalpat
APPLICANT: HUNG, Chiung-
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LENGTH: 5588
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1).7(321)
OTHER INFORMATION: SE1861:ureA:urease gamma subunit:ATCC12228:NC_004461.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 ATGAATTATTAGAAGGCGCGCGTGATGG---TAAAACGGTAGCTGAACTYATGAGCTATG 196
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TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE: PO26927W0
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SEGWIN99, version 1.03
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                    1 3.2%; Score 92.6; DB 9;
Similarity 58.7%; Pred. No. 3.5e-12;
76; Conservative 1; Mismatches 120;
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Similarity 58.3%; Pred. No. 1.6e-11;
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 12794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-471-571A-3255
. Sequence 3255, Application US/10471571A
. Publication No. US20060115490A1
. GRNERAL INFORMATION:
                                                                                                                                        TYPE: DNA ORGANISM: Staphylococcus epidermidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 176;
                                                                                                              LENGTH: 321
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APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/USO5/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
                                                                                                              DIFFERENT SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)..(315)
OTHER INFORMATION: WANOLUFWB; ORF; 0000000011100; Cluster contains WANOLUCTI
OTHER INFORMATION: :sgad_360118_2391::EGAD orf prediction:ATCC12228:NC_004461
OTHER INFORMATION: .1
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                                                                                                            DETECTING MULTIPLE STRAINS OF
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                                             APPLICANT: MULPDY, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTI)
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
FRIOR FILING DATE: 2005-10-05
FRIOR FILING DATE: 2005-10-05
FRIOR FILING DATE: 2005-10-05
FRIOR FILING DATE: 2005-10-05
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FRIOR FILING DATE: 2004-110-05
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Publication No. US20060160121A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1414 CGGCCAAATGGAACTTGCA 1432
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APPLICANT: Mounte, William M
APPLICANT: Mounte, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
TITLE OF INTERESTRATION SECPHEN
TITLE OF INTERIOR SECPHEN
TILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR APPLICATION NUMBER: PCT/USO5/035471
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: US 60/615,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               793 GATTGGCATGAACGGCCTTGTGAATAACATCGCGGATGAACGCCATAAACATAAAGCGCT 852
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                                                                                                                                                                                     APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P020927W0
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT PILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 408;
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Pred. No. 3.3e-09;
0; Mismatches 183; Indels
                                                                                                 Sequence 3277, Application US/10471571A Publication No. US20060115490A1 GENERAL INFORMATION:
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Sequence 11114, Application US/11348413

; Publication No. US20060160121A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
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Best Local Similarity 50.9%;
Matches 190; Conservative (
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LENGTH: 408
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APPLICANT: Muchts, William M
APPLICANT: Muchty, Ellen
APPLICANT: Muchted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT PAPLICATION NUMBER: 2006-02-07
PRIOR PLILING DATE: 2006-10-05
PRIOR PLILING DATE: 2005-10-05
PRIOR PLILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ DI NO 11115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(402)
OTHER INFORMATION: WANOIUFWI; ORF; 0000000011110; Cluster contains WANOIOSHN
OTHER INFORMATION: .SE1862:ureB:urease beta subunit:ATCC12228:NC_004461.1
ATGAATTATTAGAAGGTGCACGCGATGG---TAAGACCGTTGCAGAGTTAATGAGTTATG 178
                                                      GTAGACAAATTCTAAACAAAGAAGATGTCATGGATGGTGTCGAACACATGATTACAGATA 238
                                                                                                                                                                447 TAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCCCATCG 506
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                                                                                                                                                                                                                                                                                                                                                        Sequence 11115, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
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FEATURE:

NAME/KEY: misc feature
LOCATION: (1). (240)
OTHER INFORMATION: .egad_359698_2389::EGAD orf prediction:ATCC12228:NC_004461
OTHER INFORMATION: .egad_359698_2389::EGAD orf prediction:ATCC12228:NC_004461
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Kall
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 58815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
FRIOR PAPLICATION NUMBER: EP 04105479.2
PRIOR PELING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-01-03
PRIOR PLING DATE: 2004-01-03
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.3%; Score 66.2; DB 9; Length 240; Best Local Similarity 56.9%; Pred. No. 5.4e-06; Matches 119; Conservative 1; Mismatches 89; Indels
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                                                                                                                                  TYPE: DNA ORGANISM: Staphylococcus epidermidis
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SOFTWARE: PatentIn version 3.3
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 11114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-11-266-748A-58311/c
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LENGTH: 1933
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1.7%; Score 49.2; DB 8; Length 1933;

Query Match

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                                                         115 ATATTATTACTTATATAAAAGTTAATAAAAGTAACGAAATTAGGACTATAATCCCAT 174
                     Gaps
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Best Local Similarity 57.9%; Pred. No. 0.14; Matches 99; Conservative 1; Mismatches
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Search completed: August 10, 2006, 01:50:58 Job time : 447 secs

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FEATURES
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DU76294 ASNG641.9
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EX816461 Arabidops
DK637093 EST10271
DV133265 CV03067A1
DK637093 EST102404
CO122599 GR ED04F
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DK63399 EST102801
DK63393 EST102456
DR6335182 BJ EB000
CV19567 CGF100344
DV135585 CGF100344
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GenCore version 5.1.9
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υ		1.8		614	-	AZ935371		ᅼ	_
		7.4		747		CF690511		CF690511 CCAAZ91TR	
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2 5	DU750758/C								
LOCUS	707/25 TUS	DU7507	88			956 bp	DNA line	ar GSS 27-JAN-2006	9
DEF	DEFINITION	ASNF16	O I		10-	6-02 u	ed marine mi	croorganism	2
		HF130 10	90-	-02 gen	genomic	colone HF0130	019002,	genomic survey	
ACC	ACCESSION	DU750758	. 86						
VER	VERSION	DU750758	٦:	GI:8576059	605	94			
Æ	KEYWORDS	GSS.							
Soci	SOURCE	uncultured		arine	i i	roorganism HF	30 10-06-02		
 ر	OKGANISM	uncultured unclassifi		arine secue	nce	marine microorganism Hrisu_ru-ue-u ed secuences: environmental_samples	al_samples.		
REF	REFERENCE	1 (ba	ses 1 (to 956	_				
Ø	AUTHORS	DeLong	DeLong, E.F., Preston, C.M.,	Prest	g.	J.M., Mincer, T., Ric	žh, V.,	1, S.J.,	
		Frigaa	rd, r	., Mar	tını	sz,A., Sulliva	ın,m., Edward		
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Ö	COMMENT	Contac	Science (2006) in press Contact: Susan Lucas, A	an Luc	as,	Alex Copeland,	, Sam F	Alla Lapidus	
		Kerrie	Kerrie Barry, Tijana	, Tija	na (avir	Ω	, Paul Richardson	
		and Ed	and Edward DeLong	eLong		4			
		US DOE	US DOE Joint Genome US DOE Joint Genome	Genom		Institute			
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		Tel: 6	: 617-253-5271	-5271					
		Email:	PMRicl	hardso	n@]]	ol.gov: delond	r@mit.edu		
		North	Pacific	c Subt	rop		vaii) picoplankton	rton genomic fos	יס
		DNA Li	DNA library prepared from	prepar	, ed	marine p	marine picoplankton in	the o/e	_
		Coordinates:	mates:	22.45	Z	Depth Depth	130 m Temperature	· · ·	
		Salini	ty: 35	.31 psu Oxygen:	Ĝ.	cygen: 204.9 u	umol/kg		
0.00	SEATTERS	Class:	fosmic	fosmid ends.	. 6	mid ends. Ocation/Ocalifiers			

Location/Qualifiers
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Coganism="uncultured marine microorganism HF130_10-06-02"
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/db_xref="taxon:361146"
/clone="HF0130_019002"
/cell type="marine picoplankton, less than 1.8 um, greater than 0.22 um fraction"

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1785 TCCTCCACCACCACTATTCCCTATACCATTAATACGGTTGCAGAACACTTAGACATG 1844
           116 TCATCGTCTGAAAAGATATATCTCAAAGGTCACTATTAATCCTGCGATAGCTCATGGAAT
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Pred. No. 6.9e-71;
0; Mismatches 363; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unclassified sequences; environmental samples.
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/clone_lib="HF130_10-06-02"
/note="Vector: pCC1FOS; North Pacific Subtropical Gyre
/mote="Vector: pCC1FOS; North Pacific Subtropical Gyre
/maxii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 uw, greater
than 0.22 um fraction. Picoplankton collected at 130 m
depth on 10/6/2002 Coordinates: 22.45 N,158 W Sample
Date: 10/6/2002 Coordinates: 22.45 N,158 W Depth 130 m
Temperature: 22.19 C Salinity: 35.31 psu Oxygen: 204.9
umol/kg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   596 TCAACTAGACGTACAAGTTTGTATTCATACAGATACCCTAAATGAAGCTGGTTTTGTTGA
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Pred. No. 2.6e-75;
0; Mismatches 362; Indels
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Best Local Similarity 61.8%;
Matches 588; Conservative
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/organism="uncultured marine microorganism HF200_10-06-02"

mol_type="genomic DNA"

/db_xref="taxon:361147"

/clone="HF0200 0948110"

/cell type="marine picoplankton, less than 1.8 um, greater
than 0.22 um fraction"

/clone lib="HF200 10-06-02"

/note="vector: pCCIFOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 200 m
depth on 10/6/2002, Coordinates: 22.45 N 158 W. Sample
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 200 m
Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8
umol/kg"
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US DOB Joint Genome Institute
2800 Mitchell Drive Bl00, Walnut Creek, CA 94598-1698, USA
2800 Mitchell Drive Bl00, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-2579
Fax: 617-253-2679
Faxi 617-253-2
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57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             νυγ60951 SANG3437.g2 HF200_10-06-02 uncultured marine microorganism HF200_10-06-02 genomic clone HF0200_094Ε10, genomic survey sequence.
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                                                                                                                                                                                                      CAGTGCTCATGTTGGTTCGGTAGAAG-TTGAAAACTAGCAGACTTAGTGAT
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Gontact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus, Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus, Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson and Edward DeLong
US DOB Joint Genome Institute
US DOB Joint Genome Institute
US DOB Joint Genome Institute
1800 Mitchell Drive Bl00, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-5279
Email: PMRichardsonalbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
North Pacific Subtropical Gyre (Hawaii) picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 10/6/2002
Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C
Salinity: 35.04 psu Oxygen: 198.8 umol/kg

microbial communities in the ocean's interior

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                                                                                                              CTCATGACATGCCACCACCTAGACAAACGCATCCGCGAGGATTTACAATTTTCTCAAAGC
                                                                                                                                                                                                                                                          CGTATCCGCCCCGGCTCTATCGCGGCTGAAGATGTGCTCCATGATATGGGTGTGATCGCG
                                                                                                                                                                                                                                                                                                                                                                                                   ATGACAAGCTCGGATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTCCTCGAACTTGG
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/clone="HP02000 064019"
/cell type="marine picoplankton, less than 1.8 um, greater than 0.22 um fraction"
/clone lib="HP200 10-06-02"
/note="Vector: pCC1F0S; North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 200 m depth on 10/6/2002, Coordinates: 22.45 N,158 W. Sample Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8 umol/kg"

organism="uncultured marine microorganism HF200_10-06-02"

/mol_type="genomic DNA" /db xref="taxon:361147"

Location/Qualifiers

Class: fosmid ends

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TICCTITICTCCACAACAATICCCTACCGCTCTAGCCAATGCCGTTACAACCATGTTTGGA 1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CTCCGCAAAATGTACGAGGCGGTGGAGGCGTTCCCGCTCAACTTCGGCTTTTTGGGCAAG
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                                                                  Gaps
                                                               3;
   Score 335.2; DB 14; Length 942; Pred. No. 2.8e-68;
                                                            0; Mismatches 318; Indels
   11.6%;
                                                                  Matches 538; Conservative
Query Match
Best Local Similarity
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uncultured marine microorganism HF200_10-06-02
unclassified sequences; environmental samples.
1 (bases 1 to 942)
DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Hallam, S.J.,
Frigaard, N.U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S.W. and Rarl, D.M.
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ASNG641.g2 HF200_10-06-02 uncultured marine microorganism HF200_10-06-02 genomic clone HF0200_064A09, genomic survey sequence.

DU762934 DU762934.1 GI:85772770

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE

linear

DNA

942 bp

DU762934

LOCUS

RESULT 3 DU762934

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1389 GGCACGAATGCGACTACTATCACTCCGGGCAAATGGAACTTGCACCGCATGTTGCGCGCA 1448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1509 CAACTTGTAGAACAAGTAGAAGCGGGCGCGATTGGTTTTAAATTGCATGAAGACTGGGGGC 1568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 ATCATCTCCGTGGTAGAGCATCAAAATGTTCTGCCATCATCGACCAACCCTACAAGACCA 601
      approximately 1 g mycelia per 10 ml TRIzol. The cDNA widirectionally ligated into the pBlueScript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AAGATTGTGACCGCGGGCGCTATCGACACGCATATTCACTTTATCTGCCTCAGCAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTACCGCTCTAGCCAATGGCGTTACAACCATGTTTGGAGGCGGCACAGGTCCTGTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGATCAGCTTCCTATCATATTGGTATTACTGGCAAAGGTAATGATAGTTCTCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1629 TGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATGACACCCTAAATGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1809 TATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGCCACCACCTAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGAAGATGTGCTCCATGATATGGGTGTGATCGCGATGACAAGCTCGGATTCGCAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1569 ACAACACCAAGTGCGATCGATCACTGCTTGAGGGGGGGGAGATGAATACGATGTGCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 critáricacacricacecritaaceaercreecririerceaarcraecreerric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 AAGAACCGCACAATTCATAACTTATCACACAGAGGTGCAGGAGGTGGCCATGCTCCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTATCACCATGGCAGGCGAGCTCAATATTCTACCCTCCTCCACCACCCCACTATTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1989 ATGGGGCGTGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAA
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                                                                                                                                                                                                                                                                                                         1209 GATGGCGTAAGCCCTCATATGGTCGTGGGTGTGGGCACAGAAGCACTAGCAGGGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1689 AACGGGCGCCCATCCATGCCTACCACATTGAGGAGCGGGTGGAGGACACTCACCTGAT
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                                                                                                                                                                                                                                                                                                                                                                               GACGGCGTAACAGAGGGCATGGTCGTCGGAAGCTGCACGGATGTCGTAGCAGGTGAAGGA
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                                                                                                                                                                             DB 10; Length 958;
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                                                                                                                                                                         Score 333.2; DB 10; Length
Pred. No. 8.5e-68;
0; Mismatches 368; Indels
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                                                                                                                                                                             11.6%;
60.6%;
                                                                                                                                                                  Query Match
Best Local Similarity 60.63
Matches 572, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               842
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 958)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattnef, R.D., F., Comparative analysis of 87,000 expressed sequence tags from the fumonisin-producing fungus Fusarium verticillioides
Fungal Genet. Biol. 42 (10), 848-861 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGCGGATAAGAATAAAAAAAATTTGGTAAGCTTCCTGAAGATGGCAAAGATAACGAT 2087
                                                                                                                                                                                                                                           1908 ATCCGCCCCGGCTCTATCGCGGCTGAAGATGTGCTCCATGATATGGGTGTGGTCGCGATG 1967
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/clone lib="FvM"

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ATGACATGCCACCACCTAGACAAACGCATCCGCGAGGATTTACCAATTTTCTCAAAGCCGT
                                                                                                                                                                                                                                                                                                                                                                               1968 ACAAGCTCGGATTCGCAAGCAATGGGGCGTGCGAGGGAAGTGATTCCTCGAACTTGGCAG
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                                                                                                                                                               ATGGTCTGCCACCTCGCCCGCGATTCCGGAGGACGTCGCCTTTGCCGAATCGCGC
                                                                                                                                                                                                                                                                                                         Funger 16099185
Contact: Brown, D.W.
USDA/ARS/NCAUR
USDA
1815 N. University St, Peoria, IL 61604, USA
1815 N. University St, Peoria, IL 61604, USA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6689
Email: browndwencaur.usda.gov
TIGR sequence name: FVWAW64TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
Location/Qualifiers
Location/Qualifiers
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/mol_type="mRNA"
/strain="m3125"
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KEYWORDS
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AUTHORS
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PUBMED
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RESULT

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DR637093 946 bp mRNA linear EST 11-JUL-2005
EST1027718 FvM Gibberella moniliformis cDNA clone FVMAT95, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 AAGAGGGTTGTAGCGGTGTCCAACGTGAGGCAGCTCACAAAACTCGACATGAAGCTGAAT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901 gargcgcrrccagagarcaccgrggarccagagacaracgrrgrcacagcaaarggcgag 960
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Gibberella moniliformis
Gibberella moniliformis
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
1 (bases 1 to 946)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Yutterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
Comparative analysis of 87,000 expressed sequence tags from the fumonisin-producing fungus Fusarium verticillioides
                                                                                                                                                                                                                                                                                                                                                                                                                                              2006 AGTGATTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAAGATTTGGTAAGCTTCC
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181 GTGAAAATGTACTCCCGTCATCAACCAACCCAACACGCCCTATACGAAAAATACTGTA
                                                                 1827 GCAGAACACTTAGACATGCTCATGACATGCCACCTAGACAAAACGCATCCGCGAGGAT
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                                                                                               301 GTAGCTTTTGCTGAATCAAGAATAAGAGCTGAAACAATAGCTGCAGAGAGATATATTGCA
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schaother V., Weissenbach J., Salanoubat M.

URGV.INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are .assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                              CNSOABR8

Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH4ZD08 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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/db_xref="taxon:3702"
/clone="GSLTPGH4ZD08"
/tissue_type="Hormone Treated Callus"
/cocype="CO1-0"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGAAGAGTATTCTATGAATGTGGGCTTTTTTGGGCAAAGGCAATAGCTCTAGCAAAAA 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACTTGTAGAACAAGTAGAAGGGGGGGGGGGGTTGGTTTTAAATTGCATGAAGACTGGGGGC 1568
                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="mycelia"
/clone_lib="FvM"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhOI; anamorph: Fusarium verticillioides. Library
FvM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYAM culture from strain M-3125.
Cultures were vaccuum filtered and the mycelial mats were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAACGAACGCAACTTGTACGCCTGGTGCTCATTACATGCGTCAAATGTTGCAGGCG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 TGCGATCAGCTTCCTATCAATATTGGTATTACTGGCAAAGGTAATGATAGTTCTCCTGAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 GGTCTGCGCGATCAGGTCAATGCTGGTGCTTGTGGCCTCAAGCTTCATGAGACTGGGGGT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 TGCACTCCTGCTGCTATTGACGCTTGTCTCAGTGTCTGTGATGAATTCGATATTCAATGT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  criarizcacacidacaccerraaccacircidecririciceaarcraccarcecrecrire 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AAGATTGTGACCGCGGGCGCTATCGACACGCATATTCACTTTATCTGCCCTCAGCAAGTA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1g mycelia per 10 ml TRIzol. The cDNA was directionally ligated into the pBlueScript II SK(+) XR vector (CDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGGCGTAACAGAGGGCATGGTCGTCGGAAGCTGCACGGATGTCGTAGCAGGTGAAGGA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 AAGAACCGCACAATTCATACTTATCACAGAGGGTGCAGGAGGTGCCATGCTCCGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cch 11.5%; Score 330; DB 10; Length 94 al Similarity 60.4%; Pred. No. 4.9e-67; 570; Conservative 0; Mismatches 370; Indels
                                                                                                                                                                                                                                                                                      organism="Gibberella moniliformis"
    Fungal Genet. Biol. 42 (10), 848-861 (2005)
16099185
                                                                                                         1815 N. University St., Peoria, IL 61604
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVWAT95TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:117187"
                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="m3125"
                                                                                                                                                                                                                                                                                                                                                                           clone="FVMAT95"
                                               Contact: Brown, D.W. USDA/ARS/NCAUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 570; Conserva
                                                                                           USDA
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Tel: 701 239 1263

Fax: 701 239 1263

Fax: 701 239 1263

Fax: 701 239 1265

Fax: 702 230 
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                                                                                                                                                                                                                                                                                                                                                                                   1869 AAACGCATCCGCGAGGATTTACAATTTTCTCAAAGCCGTATCCGCCCCGGCTCTATCGCG 1928
                                                                                                                                      1809 TATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGCCACCACCTAGAC 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 03-OCT-2005
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CV03067A1A09.fl CV03-normalized library Buphorbia esula cDNA clone
CV03067A1A09.fl 5, mRNA sequence.
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1 (bases 1 to 809)
Anderson,J.V., Horvath,D.P., Thimmapuram,J., Liu,L., Hernandez,A., Kim,W.R. and Mikel,M.
542 ATCATCTCCGTGGTAGAGCATCAAAATGTTCTGCCATCATCGACCAACCCTACAAGACCA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    842 CAGAGGGGTTGGTTGCCGGAGGATGAGGGCACAGGGGCTGATAATGCGCG-TGTAAACGC 900
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1605 Albrecht Blvd, Biosciences Research Laboratory, Fargo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2106 TACATCTCCAAATACACTATCAACCCCGCTTTGACCCACGGCGT 2149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATGTCAGCAAGTATACTCACCCAGCTATTGCTCAGGGCTT 944
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Unpublished (2005)
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BACKWARD: ATTAACCCTCACTAAAG (T3)
Insert Length: 809 Std Error: 0.00
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Euphorbia esula
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db_xref="taxon:117187"
                                                                   781 GCTGGAAGTGCTAACTCCATTGCTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR sequence name: FVMA534TH
Seq primer: AAT TAA CCC TCA C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="FVMA534"
                                                                                                                                                                                                                                                         Gibberella moniliformis
Gibberella moniliformis
                                                                                                                                                                                                                         DR633422.1 GI:70708256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brown, D.W.
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Matches 548;
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SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TTTAAAGGGAGAACTATACATACTTATCACAGTGAAGGTGCCGGAGGTGGTCATGCTCCG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 TCACAAAGGGGATCAATTGGTCCGGGGCAATCAGATAACGATAACTTTCCGGATAAAACGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 TACATTTCTAAGTACACTATAAATCCTGCATTAGCAAATGGGTTTGCCGATTTAATTGGG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 AAACCCGAAATGGTGATTAAAGGAGGTGTAATTGCTTGGGAGACATGGGTGATCCAAAT 720
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                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGAACTACTCCTGCTGTGATAGACAACTTTTGAACGTAGCAGAAGAATATGATCTGCAG
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                                                                                                                                                                                                                                                                                                                          11.1%; Score 320; DB 10; Length 809; 62.2%; Pred. No. 1.1e-64; ive 0; Mismatches 306; Indels (
'organism="Euphorbia esula"
              /mol_type="mRNA"
/db_xref="taxon:3993"
/clone="CV03067A1A09.fl"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                            Local Similarity
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Matches 503
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/tissue type="mycelia"
/clone lib="FvM"
/clone lib anamorph Fusarium verticillioīdes Library
/clone lib anamorph Fusarium verticillioīdes Library
/clone lib anamorph Fusarium library
/clone lib and a 48-hour
/clone was prepared from pooled RNA obtained from a 48-hour
/clone was were vacuum filtered and the mycelial mats were
/clone library
/clone l
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EST1024047 FvM Gibberella moniliformis cDNA clone FVMA534, mRNA
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721 GCAAGCATCCCCACACACCCGAACCGGTGATNTCGAGGCCTATGTTTGGAGCATTTGGCAAG 780
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Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, J. Rterback, T., Smith, S., Feldilyum, T., Glenn, A.E., Plattner, R.D., Comparative analysis of 87,000 expressed sequence tags from the Fumonisin-producing fungus Fusarium verticillioides
Info99185
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Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
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/mol_type="mRNA"
/strain="m3125"
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USA

Arizona Genomics Institute
The University of Arizona
The University of Arizona
Torbes Building Room 303, Tucson, AZ, 85721-0036,
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwingegenome.arizona.edu
Plate: 04 row: F column: 01.
Location/Qualifiers

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Matches 519; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2149 TGAGCGAGTATATCGGCTCTGTGGAAGAGGGCAAGATCGCCGA-CTTGGTGGTGGTGGAAT 2207
TGCATGAAGACTGGGGCACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATG 1611
                                                                                                                                                                         AATACGATGTGCAAGTTTGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATG 1671
                                                                                                                                                                                                                                                         .672 ACACCCTAAATGCAATGAACGGGCGCGCCATCCATGCCTACCACATTGAGGGAGCGGGTG 1731
                                                                                                                                                                                                                                                                                                                                             1732 GAGGACACTCACCTGATGTTATCACCATGGCAGGCGAGCTCAATATTCTACCCTCCTCCA 1791
                                                                                                                                                                                                                                                                                                                                                                                                                             1792 CCACCCCCACTATTCCCTATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGA 1851
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                                        190 ATGATAGTTCTCCTGAGGGTCTGCGCGATCAGGTCAATGCTGGTGCTTGTGGCCTCAAGC 249
                                                                                                                          250 TTCATGAGGACTGGGGGTTGCACTCCTGCTATTGACGCTTGTCTCAGTGTCTGTGATG 309
                                                                                                                                                                                                              310 AATTCGATATTCAATGTCTTATTCACACTGACACGCTTAACGAGTCTGGCTTTGTCGAAT 369
                                                                                                                                                                                                                                                                                                 370 CTACGATCGCTGCTTTCAAGAACCGCACAATTCATATCTTATCACACAGAGGGTGCAGGAG 429
                                                                                                                                                                                                                                                                                                                                                                        490 ccaacccracaagaccarrcacacgaaracrcrccarcagacarcrccarargerrarge 549
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Gaps

1260 GGGGAAGGIAIGAITAITACCGCTGGGGGAAICGAITCACACACCCCACITCCITICICCA

10.7%; Score 309; DB 8; Length 872; 59.7%; Pred. No. 4.8e-62; vative 0; Mismatches 350; Indels

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1920 TCTATCGCGGCTGAAGATGTGCTCCATGATAGGTGTGATCGCGATGACAAGCTCGGAT 1979
                                                                     1320 CAACAATTCCCTACCGCTCTAGCCAATGGCGTTACAACCATGTTTGGAGGCGGCACAGGT 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1620 GTGCAAGTTTGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATGACACCCTA 1679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1860 CACCTAGACAAACGCATCCGCGAGGATTTACAATTTTCTCAAAGCCGTATCGGCCCCCGGGC 1919
                                                                                                                                                                                                         1380 CCTGTAGATGCCACGAATGCGACTACTATCACTCCGGGCAAATGGAACTTGCACCGCATG 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1500 AGCAAAAACAACTTGTAGAACAAGTAGAAGCGGGCGCGATTGGTTTTAAATTGCATGAA 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1560 GACTGGGGCACAACACCCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAATACGAT 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 CACCTCAGCAAGGATATTCCTCAAGATGTAGCATTTGCAGAATCAAGGATTAGGGCGGAA 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AAACCTGAAGAATACATGAATAATCAAAGCCGGAGCAATGGGACTGAAACTGCATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 GCTCCAGATATCATCAAGTATGTGGCGTTAAAAAGGTCCTCCCTTCGTCAACAAACGG
                                                                                                                                                                                                                                                                                                                                          1440 TIGCGCGCAGCAGAAGAGTATTCTATGAATGTGGGCTTTTTGGGCAAAGGCAATAGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO122599 872 bp mRNA linear EST 16-JUN-2004 GR Eb04F01.f GR ED Gossypium raimondii cDNA clone GR Eb04F01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gossypium raimondii
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Malvales, Malvaceae, Malvoideae, Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 872)
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
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Global assembly of Cotton ESTs Unpublished (2004) Contact: Rod A. Wing

TITLE JOURNAL COMMENT

Wing, R.A.

REFERENCE AUTHORS

CO122599 , CO122599.1 GI:48821286

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION

RESULT 9 CO122599

Gossypium raimondii

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1758 ATGGCAGGCGAGCTCAATATTCTACCCTCCTCCACCACCACCACTATTCCCTATACCATT 1817
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GAGATCGTCGAGGCCGGCGTTGCGGTCTCCAAGCTCCACGAGGACTGGGGCACAACGCCG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                          421 GTCTGCGAATTCAACAACGTACTGCCATCGTCCACGAACCCCACACGCCCATACGCAAAC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 748)
Coffman, J.A., Robertson, A.J., Clifton, S., Pape, D., Hillier, L.,,
Martin, J., Wylie, T., Dante, M., Meyer, R., Theising, B., Bowers, Y.,
Gibbons, M., Ronko, I., Tasgareishvili, R., Ritter, E., Kennedy, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661 GTCGGCGAGGTCGCGCGCGCGCGCGCGCCGCGAGAGATGCGCGGAGTTGCGGGGC 720
                                                                            1578 AGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAATACGATGTGCAAGTTTGTATCCAC
                                                                                                                                 241 TCAGCCATCATCAGGTGTCTTGACGTCGGAGGACGAGGACGAGGTCAATATTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 Acedaracecricaaceaegrecarrierreaegecacrarcaaegearreec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1878 CGCGAGGATTTACAATTTTCTCAAAGCCGTATCCGCCCCCGGGCTCTATCGCGGCTGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998 GCAGGCGAAGTGCATCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAAAGAATTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1638 ACCGATACAGTCAATGAGGCAGGTTATGTAGATGACACCCTAAATGCAATGAACGGGCGC
                                                                                                                                                                                                                                                                                                                                                                      1698 GCCATCCATGCCTACCACATTGAGGGGGGGGGGGGGAGGACACTCACCTGATGTTATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2058 AAGCT-----TCCTGAAGATGGCAAAGATAACGATAATTTCCGCATTAAGCGCTACATC
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Strongylocentrotus purpuratus
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Eucchinoidea, Echinoacea, Echinoida,
Strongylocentrotidae, Strongylocentrotus.
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WashU Sea Urchin BST Project
Unpublished (2004)
Contact: Dr. James A. Coffman
WashU Sea urchin BST Project
WashU Sea urchin BST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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PchrSEQ10171 Phanerochaete chrysosporium pBluescript (EccRI-XhoI)
Phanerochaete chrysosporium cDNA clone PchrSEQ10171, mRNA sequence.
                                                                        1980 TCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTGCGGGATAAG 2039
                                                                                                                                                                                                                         2040 AATAAAAAGAATTTGGTAAGCTTCCTGAAGATGGCAAAGATAACGATAATTTCCGCATT 2099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Corticiaceae; Phanerochaete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1338 CTAGCCAATGGCGTTACAACCATGTTTGGAGGCGGCACAGGTCCTGTAGATGGCACGAAT 1397
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                                                                                                                                                                                                                                                                                             782 ATGAAATCACAAAGGGGACCACTTGGTCCTGCAGACTCAGACAACGACAATCTAAGAATC 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript KS+; Site_1: XhoI; Site_2: CSEXI, ded, double-stranded cDNA. The EcoRI-XhoI-digested cDNA was ligated with EcoRI-XhoI-digested pBluescript KS+(Invitrogen Corp)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCGACGACGACGCCCGACCCGTACTACATGCGCCACATGCTCGCTGCGACAGACGGC 120
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662 ACCATTGCTGCCGAAGACATATTGCATGACACAGGGGCAATCAGCATTATATTCTTCAGAT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada
Tel: 514 848 2424 3405
Fax: 514 848 4504
Email: tsang@vax2.concordia.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phanerochaete chrysosporium (anamorph: Sporotrichum pruinosum)
Phanerochaete chrysosporium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Expressed sequence tags from Phanerochaete chrysosporium cDNA
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/clone lib="Phanerochaete chrysosporium pBluescript
(EcoRI-Xhol)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chrysosporium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Teang A
Centre for Structural and Functional Genomics
Concordia University
                                                                                                                                                                                                                                                                                                                                                                      2100 AAGCGCTACATCTCCAAATACACTATCAA 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                          842 AAACGITATATAGCAAAATACACCATAAA 870

    .889
    /organism="Phanerochaete

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/db_xref="taxon:5306"
/clone="PchrSEQ10171"
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                                                                                                                                                                                                                        /lab_host="DH10B"

/clone lib="Sea urchin EST Libl"

/clone lib="Sea urchin EST Libl"

/note="Vector: pCMVSport6.1 (Invitrogen); Site 1: Not1;

Site_2: Smal; Arrayed normalized library of full-length

Site_2: Smal; Arrayed normalized library of full-length

Site_2: Smal; Arrayed normalized library of full-length

clone Library of full-length

urchin Strongylocentrotus purpuratus, cloned into the

vector pCMVSport6.1 (Invitrogen)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATCACCCGTACATGGCAGACGGCAGATAAGATGAAGATTTTCAGAGGCAGACTGTCAG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429 AGGAAACGGGTGACAACGACAACCTAAGGGTCAAGCGTTACATTGCCAAGTACACGGTCA 488
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Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RPDOT
High quality sequence stop: 680.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTCAATATTCTACCCTCCTCCACCACCCCCTATTCCCTATACCATTAATACGGTTG
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                                                                                                                                           organism="Strongylocentrotus purpuratus"
                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:7668"
/clone="ydd29h04"
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Matches 466; Conservative
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/tissue_type="mycelia"
/clone_lib="FvM"
/clone_lib="FvM"
/clone_lib="FvM"
/clone_lib="FvM"
/note="vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
Site_2: Xhol; anamorph: Fusarium verticillioides. Library
Site_2: Xhol; anamorph: Fusarium verticillioides. Library
FvM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYAM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                 uk637386 889 bp mRNA linear EST 11-JUL-2005
EST1028011 FVM Gibberella moniliformis CDNA clone FVMAV95, mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Fungi; Asconycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 889)

1 (bases 1 to 880)

1 (bases 1 to 880)

2 (comparative analysis of 87,000 expressed sequence tags from the fumonisin-producing fungus Pusarium verticillioides
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Pred. No. 5.9e-60;
0; Mismatches 353; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1815 N. University St., Peoria, IL 61604,
Tel: 309 681 630
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FYMAV95TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
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729 TCTTTGTGTCCAAAGCAGC 747
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/strain="m3125"
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Best Local Similarity 59.5%;
Matches 524; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brown, D.W
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Matches 483; Conservative
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TGCATGAAGACTGGGGCACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATG 1611
                                                                AATACGATGTGCAAGTTTGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATG 1671
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Gibberella moniliformis
Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 796)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L. Lee, Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Comparative analysis of 87,000 expressed sequence tags from the funonisin-producing fungus Fusarium verticillioides
                    TTCATGAGGACTGGGGTTGCACTCCTGCTGCTATTGACGCTTGTCTCAGTGTCTGTGATG
                                                                                                                                                                                                 GAGGACACTCACCTGATGTTATCACCATGGCAGGCGAGCTCAAIATTCTACCCTCCTCCA
                                                                                              AATTCGATATTCAATGTCTTATTCACACTGACACGCTTAACGAGTCTGGCTTTGTCGAAT
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Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
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/tissue_type="mycalia"
/clone_lib="FvM"
/clone_lib="FvM"
/clone_lib="FvM"
/note="Westor: pBlueScript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioïdes. Library
Site_2: XhoI; anamorph: Fusarium verticillioïdes. Library
FvM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYAM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to TRIZol Reagent (Invitrogen, Carlsbad CA) at
approximately I g mycelia per 10 ml RRIZol. The CDNA was
directionally liquid into the pBlueScript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."
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                                                                                                                                                    organism="Gibberella moniliformis"
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TIGR sequence name: FVMA846TH
Seq primer: AAT TAA CCC TCA CTA AAG
Location/Qualifiers
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/clone="FVMA846"
                                                                                                                                                                                              /mol_type="mRNA"
/strain="m3125"
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/note="wecror: pBlueScript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; ananorph: Fusarium verticillioīdes. Library
SvM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYAM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to TRIZOl Reagent (Invitrogen, Carlsbad CA) at
approximately I g mycelia per 10 ml TRIZOl. The CDNA was
directionally ligated into the pBlueScript II SK(+) XR
                                                                                                                                                                                                                                                                                                                                                                               Bukaryotta; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (Bases 1 to 849)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y., Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D., Kendra,D.F., Town,C.D. and Whitelaw,C.A.

Comparative analysis of 87,000 expressed sequence tags from the tumonisin-producing fungus Fusarium verticillioides
Fungal Genet. Biol. 42 (10), 848-861 (2005)
                                                                                                                                                                                                                                        DR635599 849 bp mRNA linear EST 11-JUL-2005
EST1026224 FvM Gibberella moniliformis cDNA clone FVMAJ96, mRNA
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                                    1963 CGATGACAAGCTCGGATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTCCTCGAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector (cDNA Synthesis Kit; Stratagene)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1815 N. University St, Peoria, IL 61604,
Tel: 309 681 6230
Fax: 309 681 6689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: browndw@ncaur.usda.gov
TIGR sequence name: FVMAJ96TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
Location/Qualifiers
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/clone="FVMAJ96"
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/strain="m3125"
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BJ Ba0003020f B. japonicum BAC library Bradyrhizobium japonicum
genomic, genomic survey sequence.
A2935182
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1437 ATGTTGCGCGCAGCAGCAGAAGAGTATTCTATGAATGTGGGCTTTTTGGGCAAAGGCAATAGC 1496
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
Bradyrhizobiaceae; Bradyrhizobium.
Tomkins, J.P., Wood, T.C., Stacey, M.G., Loh, J.T., Judd, A.,
Goicoechea, J.L., Stacey, G., Sadowsky, M.J. and Wing, R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
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                                                              123 Argiriccaegcereceárcagerrectareararregrarracregeaaageraargar
                                                                                                                                                                                                                                                                                                    GAAGACTGGGGCACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAATAC
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
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Fax: 864 656 4293

Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 719.
Location/Qualifiers
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| organis="Bradyrhizobium japonicum" | mol type="genomic DNA" | strain="USDA110" | db xref="text" coli" | /db xref="text" coli" | /clone lib="B. coli" | /clone lib="B. coli" | /clone lib="B. japonicum BAC library" | /clone lib="B. giaponicum BAC library" | /clone lib="B. giaponicum BAC library" | /clone lib="Totain" |
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1 VKLITPKEQEKFLLYYAGEVA.....ADERHKHKALDKAKSHGFIK 226 **BLOSUM62** Scoring table:

2589679 seqs, 457216429 residues Gapop 4.0 , Gapext 1.0 Searched:

2589679 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* A_Geneseq_8:* 1: geneseqp19 Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

Description	238 Urease su	250 UreaseXY	241 UreaseXY	247 UreaseXY	244 UreaseXY	349 H. bizzoz	375 Helicobac	Paı		He		Ε̈́		Hel	375 H. pylori	545 Salmonell	315 A subunit	559 Helicobac	393 Helicobac	336 Helicobac	729 H. felis	371 Urease A	647 Gerbil ur
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ALIGNMENTS

RESULT 1

immunogenic fragment; antibacterial; Vaccine; Helicobacter felis. ADJ58238 standard; protein; 226 AA. Urease subunit polypeptide X. 11-JUL-2001; 2001EP-00202666. 17-JUL-2000; 2000EP-00202565. (first entry) Helicobacter felis EP1176192-A2. 06-MAY-2004 30-JAN-2002. ADJ58238; ADJ58238

Cattoli G; (ALKU) AKZO NOBEL NV. Kusters JG,

WPI; 2002-124384/17. N-PSDB; ADJ58237.

Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of vaccines.

Claim 8; SEQ ID NO 2; 76pp; English.

The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis in Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an urease X subunit polypeptide of the invention.

Sequence 226 AA;

CMHELKKOBVMPGVGNMVPDLGVBATFPDGTKLVTVNWPIBPDEHFKAGEVKFGCDKDIE 120 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180

121

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8 g

181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGFIK 226

ADJ58241 standard; protein; 226 AA

(first entry)

06-MAY-2004

ADJ58241;

UreaseXY subunit #1.

Helicobacter felis

EP1176192-A2.

1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAELMEE

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                                                                     1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDEARRGKKTVAQLMEE
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   Length 226;
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                           Indels
100.0%; Score 1181; DB 5;
100.0%; Pred. No. 2.1e-45;
ive 0; Mismatches 0;
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                         226; Conservative
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N-PSDB; ADJ58249.
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              Similarity
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Best Local S
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immunogenic fragment; antibacterial; Vaccine; Helicobacter felis.

11-JUL-2001; 2001EP-00202666 17-JUL-2000; 2000EP-00202565

Cattoli G;

Kusters JG,

WPI; 2002-124384/17. N-PSDB; ADJ58240.

vaccines

(ALKU) AKZO NOBEL NV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMHFILKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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99.1%; Pred. No. 4.5e-45;
iive 1; Mismatches 1;
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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis. Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an

ureaseXY subunit of the invention.

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Length 226;

0; Indels

99.7%; Score 1178; DB 5; 99.6%; Pred. No. 2.9e-45; iive 1; Mismatches 0;

225; Conservative

Query Match Best Local Similarity Matches 225; Conserv

Sequence 226 AA;

1 VKLTPKEQEKFLIYYAGEVARKRRAEGLKINQPEAIAYISAHIMDEARRGKKTVAQIMEE

Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of

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181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALEKAKSHGFIK 226
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LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
          CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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Pred. No. 4.5e-45;
2; Mismatches 0;
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Best Local Similarity 99.1%;
Matches 224; Conservative
                                                                                                                            ADJ58247 standard; protein;
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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis. Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an ureaseXY subunit of the invention.
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6.8e-45;
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  Ā
ADJ58244 standard; protein; 226
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Best Local Similarity 98.7°
Matches 223; Conservative
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N-PSDB; ADJ58243.
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The invention relates to an isolated nucleic acid molecule conferring on Helicobacter bizzozeronii an ability to produce urease, where the nucleic acid molecule is a urease gene cluster comprising at least one urease structural gene and at least one urease accessory gene. The nucleic acid molecule is chosen from ureA, ureB, ureE, ureG, ureH and ureI. The invention also relates to an isolated protein encoded by the nucleic acid, a vaccine for preventing onset of disease in mammals infected by H. bizzozeronii comprising a nucleic acid and a carrier, and an isolated antibody or its binding portion raised against the nucleic acid. The nucleic acids, proteins and antibodies are useful for vaccinating mammals against onset of disease caused by infection of H. bizzozeronii, which involves administering the sequences. The sequences are useful for detecting H. bizzozeronii in a sample of tissue or body fluids which involves providing a nucleotide sequence as a probe in a nucleic acid and detecting any reaction which indicates that H. bizzozeronii is present in the sample. This sequence represents the H. bizzozeronii ureA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule having urease gene cluster, and conferring on Helicobacter bizzozeronii ability to produce urease, useful as vaccine for preventing disease in mammals infected by H.bizzozeronii.
                                                                                                                             Urease; urease gene cluster; urease structural gene; urease accessory gene; ureA; Helicobacter bizzozeronii infection; antibacterial; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 23; SEQ ID NO 3; 40pp; English
                                                                                         H. bizzozeronii ureA polypeptide.
                                                                                                                                                                                                                                                                                                                       12-AUG-2003; 2003US-00639273.
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                                                    07-OCT-2004 (first entry)
                                                                                                                                                                                                       Helicobacter bizzozeronii,
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                                                                                                                                                                                                                                                                                                                                                                                             (CHAN/) CHANG Y.
(SIMP/) SIMPSON K W.
(ZHUJ/) ZHU J.
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                 ADQ37849;
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Zhu J;

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes theoremselves and the encoded proteins. The prokaryotes used are Escherichia chemical serves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, con escruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify controllers used in proliferation, to expressed proteins. The proteins can antishodies capable of binding to the expressed proteins. The proteins can entished capable of binding to the expressed proteins. The proteins can uncleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is also useful to screen for homologous collular proliferation protein. Note: The sequence data for this patent calculated format directly from Wilbo at celectronic 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic cellular proliferation protein; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٦,
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  224
                            178 EPGEKKIVELIQIGGNQRIYGFNSLVDRQADTDGKKLALKRAKEHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.4%; Score 619; DB 4; Length 238; 53.1%; Pred. No. 1.6e-19; ive 42; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
GAGQTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                             Helicobacter pylori cellular proliferation protein #188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 11468; 511pp; English.
                                                                                                                                                                            Ą.
                                                                                                                                                                            AAU35875 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207127P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-025391P.
16-FEB-2001; 2001US-0259308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001WO-US009180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0191078P
                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; drug design.
                                                                                                                                                                                                                                                                           14-FEB-2002 (first entry)
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Best Local Similarity 53.14
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-611495/70.
N-PSDB; AAS53734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001
                                                                                                                                                                                                                            AAU35875;
178
                                                                                                                                                     AAU35875
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Gaps

9

56.3%; Score 665; DB 8; Length 234; 57.3%; Pred. No. 1.2e-21; Live 39; Mismatches 52; Indel8

Conservative

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Similarity

Local Best Loca Matches

1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE

DIELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRI 177

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LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                     181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                             Disclosure; Page 70-71; 98pp; English.
                                                                                                                                                                                                              Urease; ureA gene; ureB gene; vaccine.
                                                                                                                     AAW07193 standard; protein; 238 AA
                                                                                                                                                                                                                                Helicobacter pylori; strain CPM630
                                                                                                                                                                                                                                                                                                                                                                Ackerman SK,
Ermak T,
                                                                                                                                                                                                                                                                                                               95US-00431041.
                                                                                                                                                                                                                                                                                           96WO-US005800
                                                                                                                                                                                         H. pylori urease A subunit
                                                                                                                                                                       (first entry)
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Best Local Similarity 52.7*
Matches 118; Conservative
                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                          Pappo J,
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-497373/49.
                                                                                                                                                                                                                                                                                                                                            (ORAV-) ORAVAX INC.
                                                                                                                                                                                                                                                                                                                                                                Monath TP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 238 AA;
                                                                                                                                                                                                                                                                                           25-APR-1996;
                                                                                                                                                                                                                                                    WO9633732-A1
                                                                                                                                                                                                                                                                                                                28-APR-1995;
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11-FEB-1997
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                                                 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                         61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleotide sequences encoding Campylobacter pylori-ureaseents - and derived vectors, transformants, protein, antibodies and probes, useful in diagnosis, treatment and prevention of infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The protein can be used for the prodn. of antibodies and to prepare vacchines for the prevention /treatment of C. pylori infections. See also AAR04578-81. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-ANG-2003 to correct OS field.)
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           VKLTPKEQEKPLLYYAGEVARKRKAEGLKLNQPEALAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                    181 OTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                : : |: || : || : || : || || EEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF
                                                                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR.
(INRM ) INSERM INST NAT SANTE & RECH MED.
                                                                                                                                                                                                                                                                        Part of protein with urease activity
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                                                                                                                                                                                         AAR04579 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 34; 47pp; French.
                                                                                                                                                                                                                                                                                                                                                                           88FR-00013135
                                                                                                                                                                                                                                                                                                                                                                                             88FR-00013135
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                (revised)
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                                                                                                                                                                                                                                                                                                              Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ04328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 238 AA;
                                                                                                                                                                                                                                                                                         probe.
                                                                                                                                                                                                                                                                                                                                                                         06-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                             36-OCT-1988;
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21-SEP-1990
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                                                                                                                                                                                                                                                                                          Urease;
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Urease A (AAW07193) and B (AAW07194) subunits of Helicobacter pylori are encoded by the urea the treas of chinical isolate CPM630. Vectors, e.g. pORV214 (see also AAM44351), carrying the gene locus on be used to transform host cells for the large-scale prodn. of recombinant, enzymatically inactive, multimeric urease. The urease complex induces a mucosal immune response that can treat or prevent Helicobacter, esp. H. pylori, gastroduodenal infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                          Vaccine for inducing mucosal response to Helicobacter - contg. multimeric urease complex and pref. an antibiotic, anti-secretory agent or bismuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CMHPLKKOBVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LINAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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   Kleanthous H;
Sussman I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VKLIPKEQEKFLLYYAĞEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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Soman G,
Bhagat H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.2%; Score 616; DB 2; 52.7%; Pred. No. 2.2e-19; iive 43; Mismatches 62
   Thomas WD,
Guirakhoo F,
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WO200202141-A2
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                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                           AAM49644;
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120 INEGKKAVSVKVKOVGDRPVQIGSHFHFFEVNRCLDFDREKTFGKRLDIASGTAVRFEPG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr GJ;
                                                                                                                                                                                                                                                                          Antisense; prokaryotic cellular proliferation protein; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ğ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                  Helicobacter pylori cellular proliferation protein #6.
                                 181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; SEQ ID NO 11286; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind JW,
                                                                                                                                            AAU35693 standard; protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2000; 2000US-0191078P.
25-MAY-2000; 2000US-0206848P.
25-MAY-2000; 2000US-0207272P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0259308P.
                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001WO-US009180.
                                                                                                                                                                                                                                                                                           antibacterial; drug design.
                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu EH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                           Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                            14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                            AAU35693;
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                                                                                                                            AAU35693
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1; Gaps

Length 238;

52.2%; Score 616; DB 4; Length 236 52.7%; Pred. No. 2.2e-19; .ive 43; Mismatches 62; Indels

Query Match 52.2 Best Local Similarity 52.7 Matches 118; Conservative

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reactive epitopes in a target protein; (2) eliminating and reactive epitopes in a target protein; (2) eliminating cross-reactive epitopes, and (3) verifying remaining epitopes by determining their activity in vitro and/or in vivo. The products of the invention have antibacterial, antiulcer, antiulchammatory, cytostatic, virucide, protozoacide and immunosuppressive activity. The vaccine is especially used to protect against infection by Helicobacter pylori, but more generally can be prepared from proteins from any pathogen (virus, bacterium, protozoan) or tumour, or associated with autoimmune disease. Synthetic epitopes that are more immunogenic than natural sequences can be identified, and the vaccine may have increased immunogenicity (when formulated with adjuvant) or immunotolerance (formulated without an adjuvant). This sequence represents the urease A protein PA4 described in
                                                                                                         61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                        CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Urease A; vaccine; T cell-stimulating peptide; antibacterial; antiulcer; MTC; major histocompatibility complex; epticope; antiinflammatory; cytostatic; virucide; protozoacide; immunosuppressive; pathogen; tumour; autoimmune disease; Helicobacter pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for the preparation of a vaccine based on T cell-stimulating peptide sequences. The method comprises (1) identifying potential MHC (major histocompatibility complex)-binding and
Preparing vaccine containing T cell-stimulating peptides, useful particularly for protection against Helicobacter pylori, by selecting
                                                                                                                                                                                                                                               181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                        (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meyer TF;
                                                                                                                                                                                                                                                                                                                                                                                          AAM49644 standard; protein; 238 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epitopes from target proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUL-2001; 2001WO-EP007656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2000; 2000DE-01032538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Urease A protein PA4.
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                                                                                                                                                                            GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                                                                                61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                            LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                      1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKINQPEAIAYISAHIMDEARRGKKTVAQIMEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing an immune response against Helicobacter in mammals, useful treating Helicobacter induced gastroduodenal diseases.
                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pHUR3; vaccine; helicobacter pylori infection; urease; immune stimulation; antiulcer; cytostatic; antiinflammatory; gastrointestinal-gen.; gastritis;
              Score 616; DB 5; Length 238; Pred. No. 2.2e-19;
                                                                                                                                                                                                                                                                                                   QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                      62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hylicobacter pylori Urase A protein fragment SEQ ID 4.
52.2%; Scc... 52.7%; Pred. No. 2... 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Freeman D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kleanthous H, Londono-Arcila P,
                                                                                                                                                                                                                                                                                                                                                                                                                           AEB55115 standard; protein; 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2000; 2000WO-US030191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00431705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-343379/36.
N-PSDB; AEB55112, AEB55130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                               Best Local Simitarity ....
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptic ulcer; carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori.
Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ORAV-) ORAVAX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200132014-A2
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                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                   181
              Query Match
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AEB55115
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Helicobacter induced gastroduodenal diseases, including acute, chronic or atrophic gastritis, peptic ulcer diseases (e.g. gastric or duodenal ulcers), and gastric carcinoma. Attenuated Salmonalla vector pHUR3 was constructed expressing UreA and UreB and including an B. coli AmpR gene. The present sequence represents a protein or peptide encoded by the pHUR3 plasmid. NOTB: pHUR3 is represented by both AEBS5112 and AEBS5130, the peptides expressed by pHUR3 are shown in the sequence listing to be split between AEBS5112 and AEBS5130, yet Figure 4 shows all the peptides being expressed by the one sequence, therefore all encoded peptides are cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CMHFLKKDBVMPGVGNMVPDLGVBATFPDGTKLVTVNWPIBPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein having specific region of beta-subunit urease of Helicobacter pylori, which generates antibodies that suppress proliferation and urease activity of bacteria, useful for preventing Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein having a specific region of primary structure of the beta-subunit Helicobacter pylori urease, appearing as ADS09176 (amino acids 201-338 of the beta subunit) or a sequence which generates antibodies that suppresses proliferation of H. pylori and which
                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                            8 MKCIPPKELDKIMIHYAGELAKKRKEKGIKINYVEAVALISAHIMEEARAGKKTAAELMQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRILLKPDDVMDGVASMIHEVGIEAMPPDGTKLVTVHTPIBANGKLVPGEL-FLKNEDIT
                                                                                                                                                                                                                                                                                                                                                     1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urease; alpha subunit; UreB; gastric ulcer; peptic ulcer; gastritis;
stomach cancer; vaccine; antibody; immune reaction.
                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                     Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : |: | : | : | : : : : | | | | : | | | | : | | | | | EKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF 230
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
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(FUKU-) FUKUYAMA RINSHO KENSA CENT KK.
                                                                                                                                                                                                                                                                     52.2%; Score 616; DB 4;
52.7%; Pred. No. 2.4e-19;
iive 43; Mismatches 62,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 3; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. pylori urease alpha beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS09178 standard; protein; 238
                                                                                                                                                                                          referenced to both sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003; 2003JP-00054654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003; 2003JP-00054654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Matches 118; Conservative
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                                                                                                                                                                                                                               Sequence 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2004261080-A.
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suppresses urease activity of H. pylori by an immune reaction. Also included are a gene which encodes the urease fragment, a vaccine against H. pylori comprising the urease fragment, a transformed cell transformed by introducing the gene, an antibody which recognises the urease fragment and transforming a plant by introducing the gene into the plant and making it express. The urease fragment is useful for producing blood serum containing antibodies which suppresses proliferation of H. pylori immunising a living organism (e.g. a human, cow or hen) with the urease immunising a living organism (e.g. a human, cow or hen) with the urease tragment. The fragment may be purified from cow's milk or hen eggs from transgenic animals expressing the fragment. H. pylori is thought to be a cause of gastric and peptic ulcers, gastritis and may be implicated in gromach cancer. The urease enzyme is thought to be responsible for maintaining the bacterium in the acid conditions of the stomach. The present sequence is the H. pylori urease alpha subunit.
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Sequence 238 AA;

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                                                                                                                                61 CMHPLKKDBVMPGVGNMVPDLGVBATFPDGTKLVTVNWPIBPDEHFKAGBVKFGCDKDIB 120
                                                                                                                                                   61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVFGEL-FLKNEDIT 119
                                                                                                                                                                                                 LNAGKEVTELEVTNEGPKSLHVGSHFHFFBANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                  1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                Gaps
                                  1;
DB 8; Length 238;
51.9%; Score 613; DB 8; Length 23
52.2%; Pred. No. 3e-19;
tive 44; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                     QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
               Local Similarity 52.2 tes 117; Conservative
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Query Match
                                Matches
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ADM28643 standard; protein; 238 AA (first entry) 20-MAY-2004 ADM28643; RESULT 14 ADM28643

Helicobacter pylori urease alpha subunit protein SeqID 2.

immunogenic; urease; vaccine; passive immunisation; diagnostic; antibacterial; antibody.

Helicobacter pylori.

JP2004041084-A. 12-FEB-2004 11-JUL-2002; 2002JP-00203221.

11-JUL-2002; 2002JP-00203221

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

WPI; 2004-162021/16.

New peptide useful as a vaccine against Helicobacter pylori induces an antibody response against the bacterial urease.

Disclosure; SEQ ID NO 2; 19pp; Japanese

This invention relates to a novel immunogenic peptide that induces production of antibodies against the Helicobacter pylori (H. pylori)

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The sequence of the Helicobacter felis urease ureA gene product (given in AAR67371) was compared to ureases of Helicobacter pylori (AAR67375), proteus mirabilis (AAR67376) and jack bean urease (AAR67377) and regions of homology were identified. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                            61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                 121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFFANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA from Helicobacter pylori and Helicobacter felis – used to develop prods. for detection, treatment and prevention of Helicobacter infection.
                                                                 are useful for passive immunisation and diagnostic techniques.

Furthermore, the antibacterial peptide can be used to immunise an animal in order to produce antibodies that are present within a functional food such as milk or eggs. This polypeptide sequence is the H. pylori urease alpha subunit protein of the invention.
urease protein. Specifically, it refers to a peptide antigen capable of inducing an antibody response, such that it can be used to develop a vaccine against H. pylori. The present invention describes generating monoclonal antibodies against the urease using hybridoma techniques that
                                                                                                                                                                                                                                                                                                                                                                   61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urease; ureA gene; immunogen; vaccine; diagnostic; Helicobacter felis.
                                                                                                                                                                                                                                                                                             1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                      51.6%; Score 609; DB 8; Length 238; 52.2%; Pred. No. 4.7e-19; ive 43; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : |: | : | : | : : : | | | | : | | EKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF
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(INRM ) INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR67375 standard; protein; 238 AA.
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93WO-EP003259.
                                                                                                                                                                                                      Query Match
Best Local Similarity 52.28
Matches 117; Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. pylori ureA urease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteus mirabilis.
                                                                                                                                                                        Sequence 238 AA;
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19-NOV-1993;
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22-JUN-1995
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51.5%; Score 608; DB 2; Length 238; 52.2%; Pred No. 5.26-19.
                                                       Query Match
Best Local Similarity
Matches 117; Conserv
                            Sequence 238 AA;
 field.)
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KAEGLKINQPEAIAYISAHIMDEARRGKKTVAQL	atches 117; Conservative 43; Mismatches 63; Indels 1; Gaps 1;
	1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDBARRGKKTVAQLMEE

à g à a ò 셤 ઠે Search completed: August 9, 2006, 21:23:50 Job time : 198 secs

⁶¹ GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNBDIT 119 121 INAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180 61 CMHFLKCDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120

¹⁸¹ OTRKVOLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224

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"Sequence 2, Application US/08920095; Sequence 2, Application US/08920095; Patent No. 5837240 GENERAL INFORMATION: APPLICANT: Cynthia K. Lee et al
                                                                                                                                                                                                                                                                                        US-09-338-920B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-338-920B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11,
                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
: /EMC Celerra SIDS3/ptodata/2/iaa/6-COMB.pep:*
: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*
: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
:: /EMC Celerra SIDS3/ptodata/2/iaa/PGTUS.COMB.pep:*
:: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
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1 VKLTPKEQEKFLLYYAGEVA.....ADERHKHKALDKAKSHGFIK
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-08-920-095-2

US-09-318-920B-5

PCT-0S96-05800-2

US-08-437-697-2

US-08-443-697-22

US-08-443-697-22

US-08-467-822-22

US-09-38-920B-7

US-09-38-920B-7

US-08-46-248-22

US-08-38-920B-7

US-08-46-248-25

US-08-46-248-25

US-08-46-248-25

US-08-46-248-25

US-08-467-822-26

US-09-338-920B-3

US-08-687-645B-3

US-09-134-001C-4982

US-09-134-001C-4982

US-09-134-001C-5049

US-09-134-001C-5049
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                       650591 seqs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
                                                                                                                                                                   BLOSUM62
Gapop 4.0 , Gapext 1.0
                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                                                    US-09-904-994B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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100
100
103
145
1145
1107
                                                                       August
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                                                                                                                                                                   Scoring table:
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6111
6011
6011
5578
5578
5578
5578
5578
787
287
287
2787
                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
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                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                         Database
                                                                       Run on:
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEP-DEHFKAGEV--KFGCDK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DITLINAGKHAVQLKVKNKGDRPVQVGSHFHFFEVNKLLDFDFREKAYGKRLDIASGTAVRF 177
                      23, Appl
26884, A
18, Appl
                                                   116, App
6085, Ap
29, Appli
24, Appl
24, Appl
24, Appl
4, Appli
4, Appli
                                                                                                                                             9266, Ap
10, Appl
26886, A
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EPGEEKTVELIDIGGNKRIYGFNALVDRQADHDGKKLALKRAKEKHFGTI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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US-08-467-822-23

US-08-432-697-23

US-09-252-991A-26884

US-09-602-777A-18

US-09-110-279-116

US-09-31-681A-6085

US-07-732-242C-2

US-09-328-352-5915

US-09-328-352-5915

US-08-467-822-24

US-08-467-822-24

US-08-467-822-24

US-08-467-828-24

US-08-967-513-4

US-08-1415-0010-4415
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54.8%; Pred. No. 6.9e-23;
tive 41; Mismatches 55.
                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Helicobacter heilmannii
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Best Local Similarity 54.8%
Matches 126; Conservative
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SEQ ID NO 5
LENGTH: 238
                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKINQPEAIAYISAHIMDEARRGKKTVAQLMEE
  MULTIMERIC, RECOMBINANT UREASE VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 238;
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Patent No. 6709851
GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06132/02302
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR FILING DATE: 1005: 14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Indels
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                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.2%; Score 616; DB 1; 52.7%; Pred. No. 8.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,163
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/431,041
FILING DATE: 28-ARR-1995
ATTORNEY/AGENT INFORMATION:
                                                                 E: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             STATE: ....
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
TTYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 52.7
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-920-095-2
TITLE OF INVENTION: MU
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                   STREET:
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61 CMHFLKKDBVMPGVGNMVPDLGVBATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                                                                                                                                                                                                                                                                           121 INAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                  1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9605800
GENERAL INFORMATION:
APPLICANT: OraVax, Inc.
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATE:
APPLICATION NUMBER: PCT/US96/05800
                                                                                       52.2%; Score 616; DB 2; 52.7%; Pred. No. 8.6e-22; iive 43; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06132/020001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-APR-1996
CLASSIPICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,041
FILING DATE: 28-APR-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/568,122
FILING DATE: 06-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELECOMMUNICATION INFORMATION
TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                            Best Local Similarity 52.7%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein PCT-US96-05800-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 225 FORTY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BOE
STATE: MA
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                                              US-09-338-920B-5
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APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: IMMUNOSENIC COMPOSITION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
TUTLE OF INVENTION: 44
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 INAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.7%; Score 611; DB 1; Length 237; 52.7%; Pred. No. 1.5e-21; tive 43; Mismatches 61; Indel8
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                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CUREMY APPLICATION DATA: APPLICATION NUMBER: US/08/467,822 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-432-697-22
; Sequence 22, Application US/08432697
; Patent No. 6248330
          Ferrero, Richard L.
                                                                                                                                                                                                                                                 STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 408-4000
                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 237 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.7%
Matches 118; Conservative
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                                                                                                                                                                                                           61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                       61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                                                                                                                                          121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFRANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                        61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                           1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60
                                                                                                                                     67
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: includes sequences from Salmonella typhimurium and ; OTHER INFORMATION: Helicobacter pylori.
US-09-431-705-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: Reanthous, Patricia
APPLICANT: Londono-Arcila, Patricia
APPLICANT: Freeman, Donna
TITLE OF INVENTION: Use of salmonella vectors for
TITLE OF INVENTION: Vaccination against helicobacter infection
FILE REFERENCE: 06132/060001
CURRENT APPLICATION NUMBER: US/09/431,705
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
     Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.2%; Score 616; DB 2; Length 245; Best Local Similarity 52.7%; Pred. No. 9.2e-22; Matches 118; Conservative 43; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
     ; Score 616; DB 5;
; Pred. No. 8.6e-22;
43; Mismatches 62
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Patent No. 5843460
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09431705
Patent No. 6585975
52.2%;
52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                        Matches 118; Conservative
                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-467-822-22
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US-09-431-705-4
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          Query Match
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Gaps

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APPLICANT: Sauerbaum, occ...
APPLICANT: Sauerbaum, occ...
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNGERIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
ANDRESSEE: Dunner
ANDRESSEE: Dunner
ANDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTFIEANGKLVPGEL-FLKNEDIT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VKLIPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.7%; Score 611; DB 2; Length 237; 52.7%; Pred. No. 1.5e-21; Live 43; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 EEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF 222
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                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REPERENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/08466248
Patent No. 6258359
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Suerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 amino acids
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Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-432-697-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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IMMUNOGENIC COMPOSITIONS AGAINST
HELICOGRACTER INFECTION, POLYPEPTIDES FOR USE IN THE
COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
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                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                     AUDKESSEE:
AUDKESSEE:
AUDKESSEE:
CITY: Washington
STATE: 1300.
STATE: 0.C.
CCUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUW TYEE: F10PDy disk
COMPUTER READABLE FORM:
MEDIUW TYEE: TOPDy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RC-BOS/MS-DOS
SOFTWARE: PATCHIN BC-BOS/MS-DOS
SOFTWARE: PATCHIN DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION HAR:
APPLICATION NUMBER: US/08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION NUMBER: US/08/432,697
FILING DATE: 03-MAY-1995
CLASSIFICATION NUMBER: US/08/432,697
FILING DATE: 03-MAY-1995
CLASSIFICATION NUMBER: US/08/432,697
FILING DATE: 03-MAY-1995
CLASSIFICATION NUMBER: 03-146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.7%; Score 611; DB 2;
52.7%; Pred. No. 1.5e-21;
vative 43; Mismatches 61
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Patent No. 6709511
GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 52.74
Matches 118; Conservative
TITLE OF INVENTION: IMMU
TITLE OF INVENTION: HELLI
TITLE OF INVENTION: COME
TITLE OF INVENTION: POLY
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                             Dunner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                             ADDRESSEE:
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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Serrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INPECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
  1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

48.9%; Score 578; DB 1; Length 237;
Best Local Similarity 50.4%; Pred. No. 6.2e-20;
Matches 113; Conservative 43; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..237
OTHER INFORMATION: /note= "URE A - FIGURE 3."
                                                                                    192 GSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                     REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-JUN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/432,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  Sequence 20, Application US/08467822 Patent No. 5843460 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1300 I Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1300 I St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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TOPOLOGY: lir
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APPLICANT: Seligi, Luc
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: COllection of Prokaryotic DNA for Two-Hybrid System, Helicobacter
TITLE OF INVENTION: Collection of Prokaryotic DNA for Two-Hybrid System, Helicobacter
TITLE OF INVENTION: Dylori Protein-Protein Interactions and Applications thereof
CURRENT APPLICATION NUMBER: US/10/012,819
CURRENT FILING DATE: 1209-1-10-30
PRIOR APPLICATION NUMBER: EP 99401066.8
PRIOR APPLICATION NUMBER: EP 99401066.8
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GRILLKPDDVMDGVASMIHEVGIBAMFPDGTKLVTVHTFIEANGKLVPGEL-FLKNBDIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 PGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIELNAGKEVTELE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                51.6%; Score 609; DB 2; Length 238;
52.2%; Pred. No. 1.9e-21;
Live 43; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 49.0%; Score 579; DB 2; Length 228; Best Local Similarity 52.1%; Pred. No. 5e-20; Matches 111; Conservative 41; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thomas, William D., Jr.
APPLICANT: Monath, Thomas P.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06132/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR PELICATION NUMBER: US 08/928,081
PRIOR FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 154, Application US/10012819
Patent No. 6916615
GENERAL INFORMATION:
APPLICANT: Legrain, Pierre
                                                                                                                                                                                                                                                                  ; SEQ ID NO 7
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-338-920B-7
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Best Local Similarity 52.24
Matches 117; Conservative
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US-10-012-819-154
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LENGTH: 228
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibereo, Joan-Michel
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION:
COMPOSITIONS
TITLE OF INVENTION:
ALTER OF INVENTION:

                                                                  61 CMHPLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                          121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                       1 MKLTPKELDKLMLHYAGRLABERLARGVKLNYTEAVALISGRVMEKARDGNKSVADLMQE 60
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COUNTRY: UGA
COUNTRY: UGA
ZIP: 20005-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
TTING ADDITE: 02-MAY-1995
TTING ADDITE: 02-MAY-1995
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OTHER INFORMATION: /note= "URE A - FIGURE.3.
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REGISTRATION NUMBER: 25,146
REFERENCE, DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08432697
Patent No. 6248330
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1300 I Street, N.W.
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TELEFAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSE: Filmegan, H
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Best Local Similarity
Matches 113; Conserv
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US-08-432-697-20
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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Schard in
APPLICANT: Ferrero, Richard in
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                            61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                          121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                     181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
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MEDIUM TYPE: Floppy disk
COMPUTER: ISPO POWDATIBLE
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
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ADDRESSEE: Dunner
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ER: 03495.0137-02000
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; OTHER INFORMATION: /note= "URE A
US-08-466-248-20
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Patent No. 6258359
GENERAL INFORMATION:
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 20:
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   Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas P.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REPERENCE: 0613Z/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
SEQ ID NO 9
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Patent No. 6709851
GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas P.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
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 48.9%; Score 578; DB 2;
50.4%; Pred. No. 6.2e-20;
tive 43; Mismatches 67,
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                 Best Local Similarity ....
Matches 113; Conservative
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Matches 112; Conservative
Query Match
Best Local Similarity
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TYPE: PRT
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73 GVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGE--VKFGCDKDIELNAGKEVTEL 130
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                                                                                                                                                                                             Length 213;
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                                                                                                                                                                                          46.9%; Score 554; DB 2; 52.3%; Pred. No. 7.1e-19; tive 37; Mismatches 61;
completed: August 9, 2006, 21:30:35
ne : 51 secs
                                                                                                                                  TYPE: PRT
ORGANISM: Helicobacter mustelae
US-09-338-920B-13
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Matches 113; Conservative
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US-09-904-994B-2
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69134, A
45038, A
48209, A
55507, A
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11468, Appl
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| BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| BMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-904-994B-1

US-09-904-994B-1

US-10-639-273-3

US-10-639-273-34

US-10-35-977-8629

US-10-35-977-8629

US-10-35-977-8628

US-10-639-273-37

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US-10-282-122A-6928

US-10-282-122A-6921

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US-10-21-282-122A-6821

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                                                                                                                                                                                                                 2097797 seqs, 463214858 residues
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Maximum Match 100%
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Sequence 49772., A
Sequence 11745, A
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Sequence 60250, A
Sequence 62539, A
Sequence 56822, A
Sequence 56842, A
Sequence 11047, A
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Sequence 6838, A
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US-10-315-977-8627
US-10-424-599-254635
US-10-426-115-201340
US-10-425-115-201340
US-10-22-122A-49772
US-10-815-122A-69772
US-10-10-56-761-14633
US-10-282-122A-66250
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US-09-904-994B-14
Sequence 14, Application US/09904994B
Sequence 14, Application US/09904994B
PUBLICATION NO. US20040005325A1
APPLICANT: AKZO NO. US20040005325A1e1 N.V.
TILE OF INVENTION: Helicobacter vaccine
FILE REFERENCE: Degoedesequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
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TITLE OF INVENTION: Helicobacter vaccine
FILE REFERENCE: Degoedesequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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US-09-904-994B-2
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Best Local Similarity 100.
Matches 226; Conservative
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99.1%; Pred. No. 6.6e-42;
tive 1; Mismatches 1;
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                                                                                                          Query Match
Best Local Similarity 99.6%;
Matches 225; Conservative
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Matches 224; Conservative
SOFTWARE: Patentin Ver. SEQ ID NO 14 LENGTH: 226 TYPE: PRT
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Best Local Similarity 99.1%; Pred. No. 6.6e-42;
Matches 224; Conservative 2; Mismatches 0;
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; Publication No. US20040005325A1
; GENERAL INFORMATION:
; APPLICANT: AKZO No. US20040005325A1e1 N.V.
; TITLE OF INVENTION: Helicobacter vaccine
; FILE REPERENCE: Degoedesequenties
; CURRENT APPLICATION NUMBER: US/09/904,994B
; UNMER OF SEQ ID NOS: 21
; SEQ ID NO 8
TITLE OF INVENTION: Helicobacter vaccine FILE REFERENCE: Degoedesequenties CURRENT APPLICATION NUMBER: US/09/904,994B CURRENT FILING DATE: 2001-07-13 NUMBER OF SEQ ID NOS: 21 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                 US-09-904-994B-11
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US-09-904-994B-8
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RESULT

Sequence 11, Application US/09904994B
Publication No. US20040005325A1
GENERAL INFORMATION:
APPLICANT: AKZO No. US20040005325A1e1 N.V.

US-09-904-994B-11

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Sequence 11468, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
US-09-815-242-11468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-815-242-11468
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                 118
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Publication No. US2004014234341

GENERAL INFORMATION:

APPLICANT: Chang, Yung-Fu

APPLICANT: Chang, Yung-Fu

APPLICANT: Almpson, Kenneth W

APPLICANT: Zhu, Jiaqian

CURRENT APPLICANTON NUMBER: US/10/639,273

CURRENT PILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-16

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 34

LENGTH: 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKA-GEV--KFGCDK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GRTLLKADDVMPGVAHMIHEVGIEANFPDGTKLVTIHTPVEDGGHKLAPGEVILK---NE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 DIELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chaig, Yung-Fu
APPLICANT: Chaig, Yung-Fu
APPLICANT: Chaig, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Shupson, Kenneth W
APPLICANT: Shupson, Shup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 EPGEKKTVELIQIGGNORIYGFNSLVDROADTDGKKLALKRAKEHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 54.0%; Score 638; DB 4; Length 234; Best Local Similarity 54.8%; Pred. No. 8.1e-19; Matches 126; Conservative 41; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 665; DB 4;
Pred. No. 5.6e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Helicobacter bizzozeronii
Sequence 3, Application US/10639273
Publication No. US20040142343A1
GENERAL INFORMATION:
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; ORGANISM: Helicobacter heilmannii
US-10-639-273-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.33
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
LENGTH: 234
TYPE: PRT
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61 CMHPLKKDEVMPGVGNMVPDLGVEATPPDGTKLVTVNWPIEP-DEHFKAGEV--KFGCDK 117
                                                                                                                                                             DIELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTFIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                61 GRILLKADDVMPGVAHMIHEVGIEAGPPDGTKLVTIHTPVEAGSDKLAPGEVILK--NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                                                                                                                                                 178 GAGQTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAK-SH-GFI 225
                                                                                                                                                                                                                                                                                 Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFRENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR PELING DATE: 2000-05-23 PRIOR PELING DATE: 2000-05-23 PRIOR PELING DATE: 2000-05-26 PRIOR PLING DATE: 2000-05-26 PRIOR PLING DATE: 2000-10-23 PRIOR PLING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR PLING DATE: 2000-11-27 PRIOR PLING DATE: 2000-11-27 PRIOR PLING DATE: 2000-12-22 PRIOR PLING DATE: 2001-02-16
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Best Local Similarity 53.1%; Pred. No. 5.6e-18;
Matches 119; Conservative 42; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                   APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.4%; Score 619; DB 4;
53.1%; Pred. No. 5.6e-18;
tive 42; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature

LOCATION: (B) LÖCATION 1...238

SEQUENCE DESCRIPTION: SEQ ID NO: 8629:

US-10-335-977-8629
                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                               & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COMpatible
                Sequence 8629, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617)227-7400
TELEFAX: (617)424-414
INFORMATION FOR SEQ ID NO: 8629:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               ADDRESSEE: LAHIVE & COC
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 238 amino acids
                                                                                                                                                        NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.1<sup>1</sup>
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: UNIX
                                                                                                                                                                                                                                  CITY: Boston
JS-10-335-977-8629
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
FILE REPERENCE: 19603/3881
CURRENT APPLICATION NUMBER: US/10/639,273
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; Pred. No. 7.5e-18;
43; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION INDERS: US/09/815,242 CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-26 PRIOR PRIOR FILING DATE: 2000-05-26 PRIOR PRIOR PILING DATE: 2000-05-26 PRIOR PRIOR PILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: 60/203,525 PRIOR FILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/253,931 PRIOR PILING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR PILING DATE: 2000-12-22 PRIOR PRIOR PILING DATE: 2000-12-22 PRIOR PRIOR PILING DATE: 2000-12-16 PRIOR PILING DATE: 2001-22 PRIOR PRIOR PILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11286
LENGTH: 238
Sequence 11286, Application US/09815242
Patent No. US20020061569A1
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                                                                                                          APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu. H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Helicobacter pylori
US-09-815-242-11286
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Best Local Similarity 52.7%;
Matches 118; Conservative 4
                                                                                          APPLICANT: Haselbeck, Robert
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US-10-012-819-154
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                                                       FEATURE
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LENGTH: 228
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELLCOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                   51.2%; Score 605; DB 4; Length 237; 52.2%; Pred. No. 2.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                        62; Indels
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COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPEATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dcc-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                        43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
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FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CURRENT FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: 60/404,337
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 36
ITYPE: PRT
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TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8628:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: protein
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                                                                                                                                               ORGANISM: Helicobacter pylori
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Best Local Similarity
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APPLICANT: Legrain, Pierre
APPLICANT: Selig, Luc
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: Collection of Prokaryotic DNA for Two-Hybrid System, Helicobacter
TITLE OF INVENTION: pylori Protein-Protein Interactions and Applications thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDITINEGKKAVSVK 120
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                                                                                                                                                                                                                                                                                                                                                                        2 MIHYAGELARKRKEKGIKLNYVEAVALISAHIMEEARAGKKTAAELMQEGRTLLKPDDVM
                                                                                                                                                                                                                                                                                                                                               12 LLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEECMHFLKKDEVM
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                                                                                                                                                                                                                                        DB 4; Length 228;
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                                                                                                                                                                                                                                  Query Match 49.3%; Score 582; DB 4; Length 22
Best Local Similarity 52.6%; Pred. No. 2e-16;
Matches 112; Conservative 40; Mismatches 60; Indels
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; LOCATION: (B) LOCATION 1...228
; SEQUENCE DESCRIPTION: SEQ ID NO: 8628:
US-10-335-977-8628
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CURRENT APPLICATION NUMBER: US/10/012,819
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: EP 99401066.8
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 278
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 154, Application US/10012819
Publication No. US20030017478A1
GENERAL INFORMATION:
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ORGANISM: Helicobacter pylori
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Best Local Similarity
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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APPLICANT: Simpson, Kenneth W
APPLICANT: Zhu, Jiaqian
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
                                                                                                   APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Zhu, Jiaqian
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII WEASE GENES AND THEIR USES
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII WEASE GENES AND THEIR USES
TITLE OF INVENTION: HE DIAGNOSTIC AND TREATMENT METHODS
CURRENT APPLICATION NUMBER: US/0639, 273
FRIOR APPLICATION NUMBER: 60/404, 337
PRIOR FILING DATE: 2002-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.4%; Score 572; DB 4; Length 237; 50.0%; Pred. No. 5.8e-16; Live 43; Mismatches 68; Indels
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49.3%; Pred. No. 2.5e-15;
tive 45; Mismatches 62; Indels
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CURRENT APPLICATION NUMBER: US/10/639,273
CURRENT FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: 60/404,337
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
                      Sequence 35, Application US/10639273
Publication No. US20040142343A1
GENERAL INFORMATION:
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ORGANISM: Helicobacter hepaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter felis
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Best Local Similarity 49.3$
Matches 113; Conservative
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Best Local Similarity 50.04
Matches 112; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
LENGTH: 237
US-10-639-273-35
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LENGTH: 225
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1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60

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180 VFDRQRAYGWRLNIPAGTAVRFEPGDAKTVTLVSIGG-RKVIRGGNGIADGAVNRSQLNB
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224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Oryza sativa
US-10-449-902-47195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALDKAKSHGF
US-10-449-902-47195
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29544, A
33134, A
40435, A
98802, A
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460.985 Million cell updates/sec
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1: /BMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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8: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Sequence
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                  GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-449-902-56037

US-11-056-355B-60475

US-11-056-355B-60475

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-10-953-349-33825
-11-292-431-37
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1110040, A 621004, A 3192, A D 141120, A D 141120, A D 141120, A D 141130, A D 53288, A 5581, A D 5481, A D 88013, A B 8013, A
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Toundation for Advancement of International Science.
ITLE REPRESINCE: MOA-A020SY1-US
FILE REFERENCE: MOA-A020SY1-US
CURRENT FILING DATE: 2003-05-29
PRIOR PAPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
LENGTH: 843
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US-11-056-355B-40434

US-11-056-355B-98801

US-11-056-355B-62104

US-11-056-355B-62103

US-11-056-355B-62102

US-11-056-355B-62102

US-11-056-355B-62102

US-11-056-355B-14120

US-10-449-902-51702

US-11-056-355B-14119

US-10-449-902-532B5

US-11-056-355B-14118

US-10-449-902-532B5

US-11-330-403-426

US-11-330-403-5481

US-11-330-403-5481

US-11-330-403-5481

US-11-356-355B-880113

US-11-056-355B-880113
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36.9%; Score 436; DB 6;
Best Local Similarity 37.6%; Pred. No. 2.2e-08;
Matches 94; Conservative 48; Mismatches 80,
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Publication No. US20060123505A1
GENERAL INFORMATION:
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 4025-2
SOFTWARE: PATENTIN VERSION 3.3
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                                                                                                                                                                                                                           60 GKE-M--LGRRHVLPSVVATLKQVQVEGTFPTGTNLITVVNPVCSDDGDLEKALYGSFLP
                                                                                                                                                                                                                                                                                                                                                                                   147 HFFEANKALKFDREKAYGKRLDIPSGNTLRIGAGQTRKVQLIPLGGSKKVI-GMNGLVNN
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Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
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                                                                                                                                                                               59 - BECMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVT-VN-
  Similarity 36.1%; Pred. No. 5.6e-06; 95; Conservative 42; Mismatches 78;
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; Sequence 33836, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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US-10-953-349-33826
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Best Local Similarity 33.3%
Matches 69; Conservative
Best Local Similarity
Matches 95; Conserv
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION NUMBER: 105/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 33825
LENGTH: 841
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APPLICANT: XUE, Jiah-Juen
TITLE OF INVENTION: Attenuated Vaccine Useful for
TITLE OF INVENTION: Immunizations Against Coccidioides spp. Infections
FILE REFERENCE: 529522000600
CURRENT APPLICATION NUMBER: US/11/292,431
PRIOR APPLICATION NUMBER: US 60/633,399
PRIOR FILING DATE: 2005-12-02
PRIOR FILING DATE: 2004-112-03
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FREEEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.0%; Score 401; DB 6; Length 841; 36.4%; Pred. No. 5.3e-07; tive 45; Mismatches 86; Indels
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                                                                                                   Sequence 33825, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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LENGTH: 836
TYPE: PRT
ORGANISM: Coccidioides posadasii
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Zea mays subsp. mays US-10-953-349-33825
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SESHAN, Kalpathi
HUNG, Chiung-Yu
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239 VMQKVNANSF 248
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Matches 91; Conserv
                                                                              US-10-953-349-33825
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR PLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
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Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 -LD----KAKSHGFIK 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Conservative
                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Oryza sativa
US-10-449-902-31438
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LENGTH: 936
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Best Local S
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Publication No. US20060115490A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: PO26927W0
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR APPLICATION NUMBER: GB-0107661.1
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SEQWIN99, version 1.03
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Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
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; OTHER INFORMATION: urease gamma subunit US-10-471-571A-3256
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CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SEQWIN99, Version 1.03
SEQ ID NO 3256
                                                                                                                                                                                                                 ORGANISM: Staphylococcus aureus
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Matches 54; Conserva
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPERENCE: MOA-AO2051: US.
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
## APPLICANT: Foundation for Advancement of International Science.
### TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
### FILE REPERENCE: MOA-A0205YI-US
### CURRENT APPLICATION NUMBER: US/10/449,902
### CURRENT FILING DATE: 2003-65-29
### PRIOR APPLICATION NUMBER: UP 2002-203269
### PRIOR PILING DATE: 2002-05-30
### PRIOR PILING DATE: 2002-05-30
### PRIOR PILING DATE: 2002-12-11
### NUMBER OF SEQ ID NOS: 56791
### SEQ ID NO 31438
### LENGTH: 876
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Best Local Similarity 24.2%; Pred. No. 7.7e+02;
Matches 62; Conservative 45; Mismatches 95.
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                                                                                                                                         117 KDIELNAGKEVTELEVTNEGPKSLHVGS-HFHFFEANKALKFDREKAYGKRLDIPSG--N 173
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                                                                                                                                                                                                                                                                                                                                                                                                                               TLRI-GAGQTR-KVQLIPLGGS--KKVIGMNG------LVNNIADER-HKHKA--- 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 MEKINDVTHSIKKAVGLEAAESIGE-KVLEKGEOK------AASKAAKEGLEKVVE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAYGKRLDIPSGNTLRIGAGOTRKVQLIPLG-----GSKKV--IGMNGLVNNIADBRHKH 213
576 YFSGSL--KDAAKSLGV-CPTTLKRICRHHGISRWPSRKINKVNRSLKKI-QTVINSVHG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OP INVENTION: Polypeptides Encoded Thereby
FILE REPERBYCE: 2750-1590F023
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT APPLICATION NUMBER: US/11/056,355B
PRIOR APPLICATION NUMBER: 06/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ. ID NOS: 119966
SEQ ID NO 60476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88; Indels
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| LOCATION: (1)..(327)
| OTHER INFORMATION: Ceres Seq. ID no. 15169774
| US-11-056-355B-60476
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29.3%; Pred. No. 85;
tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 60476, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LD----KAKSHGFIK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805 MTDSSSGSASSHPTFK 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KA--L-DKAKSHGFIK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          зо4 каоньсектокнаник з19
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ORGANISM: Glycine max
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Best Local Similarity
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JS-11-056-355B-60476
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Sequence 60475, Application US/11056355B Publication No. US20060150283A1

US-11-056-355B-60475

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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENTIN VEFSION 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 KASGMTLETVAG---PIGAKIABKV----AGKAASKGIKEAQEKGLNDAVGDLAEE-IKE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 QSKQLKYYTGNFDQYCQTRSE-LEBNQMKQYRWEQEQISHMKEYIARFGHGSAKLARQAQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AQLMEECMHFLKKDE-VMPGVGNMVPDL-GV--EATFPDGTKLV--TVNWPIEP--DEHF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 --KAGEVKFGCDKDIELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALK--FDR--E 160
           APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS.
CURRENT APPLICATION NUMBER: US/11/056,355B
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2005-02-14
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 MEKINDVTHSIKKAVGLEAAESIGE-KVLEKGEQK------AASKAAKEGLEKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 VKGTTYDKVSDAIKHKLDDAGNVIQ----EGLD-RAKEAI-HRATHTTQEGVQETG-NTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAYGKRLDIPSGNTLRIGAGQTRKVQLIPLG-----GSKKV--IGMNGLVNNIADERHKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VKLT--PKEQE--KFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEA--RRGKKTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(336)
; OTHER INFORMATION: Ceres Seq. ID no. 15169773
US-11-056-355B-60475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.3%; Score 169; DB 29.3%; Pred. No. 90; tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 6491, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || | :| : | |
313 KAQHLGEKIQKHAHHK 328
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US-10-953-349-6491
Vyacheslav
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Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                     TYPE: prt
ORGANISM: Glycine max
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Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: peptide
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LENGTH: 336
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LENGTH: 508
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49 RGKKTVAQLMEE--CMHFLKKDEVM----PGVGNMVPDL--GVEATFPDGTKLVTVNWPI 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 HF----FEANKALKFDRE-KA--YGKRLDIPSG---NTLR--IGA-GQTRKVQLIPL--- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 QEKFLLYYAGEVAR--KRKAEGLKLNQ------PEAIA----YI-----SAHIMDEAR 48
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TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1290FUSZ
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
LENGTH: 508
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS.
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 33135
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Best Local Similarity 29.2%; Pred. No. 3.1e+02;
Matches 80; Conservative 33; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 --GGSKKVIGMNGLV----NN-IADERHKHKALD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: peptide
; LOCATION: (1)..(508)
; COCATION: (1)..(508)
US-11-056-355B-33135
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OTHER INFORMATION: Ceres Seq. ID no. 13497309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40436, Application US/11056355B bublication No. US20060150283A1 GENBEAL INFORMATION:
APPLICANT: Brover, Vyacheslav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: prt
ORGANISM: Arabidopsis thaliana
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US-11-056-355B-40436
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Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 29545
LENGTH: 508
            49 RGKKTVAQLMEE--CMHFLKKDEVM----PGVGNMVPDL--GVEATFPDGTKLVTVNWPI 100
                                                               :||:|: || : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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OTHER INFORMATION: Ceres Seq. ID no. 13497309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Mismatches
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ORGANISM: Arabidopsis thaliana
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Matches 80; Conserv
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US-11-056-355B-29545
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Query Match

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101 EPDEH--FWAGEVKFGCDKD--IEL---N-AGKEVTELE-VTNEGPKSLH-----VGSHF 146
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                                49 RGKKTVAQLMEE--CMHFLKKDEVM----PGVGNMVPDL--GVEATFPDGTKLVTVNWPI 100
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8 QEKFLLYYAGEVAR--KRKAEGLKLNQ------PEAIA----YI-----SAHIMDEAR 48
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APPLICANT: Brover, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-14
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 98803
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| LOCATION: (1)..(508)
| OTHER INFORMATION: Ceres Seq. ID no. 13601531
| US-11-056-3558-98803
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Job time : 35 secs
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ORGANISM: Arabidopsis thaliana
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OM protein - protein search, using sw model

August Run on:

9, 2006, 21:24:06; Search time 40 Seconds (without alignments) 543.625 Million cell updates/sec

US-09-904-994B-2 1181 1 VKLTPKEQEKFILYYAGEVA......ADERHKHKALDKAKSHGFIK 226 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 4.0 , Gapext 1.0

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ease		m.	urease, beta/gamma	urease (EC 3.5.1.5	probable urease F1	m		urease (EC 3.5.1.5	probable ureA prot	probable urease st	urease gamma subun	urease (EC 3.5.1.5	urease (gamma subu	urease (EC 3.5.1.5	ښ	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease gamma subun	'n.	m.	urease (EC 3.5.1.5	urease gamma subun	urease (beta subun	ğ	urease (EC 3.5.1.5	urease gamma subun	urease gamma subun	urease damma chain
SUMMARIES		B71977	URKCAP	S35290	D75586	URJB	A96699	T29055	T37939	A36138	H70664	D85603	B90794	S74889	B69729	A36950	S47102	538484	A64076	C90027	B47090	S08478	B43719	E83037	C69729	AD2264	S42602	D83681	AE2872	F97648
	DB	2		Н	~		~	~	~	-	N	7	~	N	~	~	N	-	N	N	~	-	-	~	~	7	N	~	~	~
	Length	238	238	237	228	840	838	227	835	100	100	100	100	100	105	100	100	137	100	100	100	100	100	100	124	100	100	100	100	107
	Query Match	52.4	52.2	48.4	43.3	39.1	36.2	35.2	34.9	24.3	24.0	24.0	24.0	23.9	23.7	ë.	23.3	23.2	23.1	22.9	22.9	22.7	22.6	22.6	22.6		ς.	٠	21.8	21.8
	Score	619	616	572	511	462	427	416	412	287	284	283	283	282	280	276	275	274	273	271	270	268	267	267	267	265	263	262	257	257
	Result No.	1	2	٣	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

urease (BC 3.5.1.5) 26K chain - Helicobacter pylori (strains 26695 and others) NyAlternate names: urea amidohydrolase; urease alpha chain C;Species: Helicobacter pylori C;Species: 30-Sep-1991 #sequence revision 15-Aug-1997 #text change 09-Jul-2004 C;Accession: A38537; A64529; S07884; B35306; A41502; A61371; E49215

urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease beta chain	urease (EC 3.5.1.5	urease beta subuni	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease beta subuni	urease (BC 3.5.1.5	urease (BC 3.5.1.5	urease (EC 3.5.1.5	hypothetical prote	urease complex com	urease complex com	urease (EC 3.5.1.5	urease (EC 3.5.1.5
S47103	S31418	AE2264	S38483	D90027	AB3333	AI0324	AC2872	831417	S42604	AC3333	S76224	H82890	A82891	T50709	T50708
2	1	9	2	2	6	2	7	2	٦ ا	2	3	4	1 2	8	7
12(16,	õ	10	13	15.	100	.01	10:	51	10	<u>0</u>	15,	10.	138	10(
21.8	21.8	21.5	21.3	21.3	21.1	21.0	20.6	20.6	20.4	20.2	20.2	20.1	20.0	20.0	19.8
57	257	254	252	252	249	248	243	243	241	238	238	237	236	236	234
7					•										

ALIGNMENTS

RE P7	RESULT 1
i i i i	urane alpha chain - Helicobacter pylori (strain J99) C.Species: Helicobacter pylori A.Variatio, errain Joa
:0:	C.bata: 07. Strain 07. C.bata: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C.brossion: R71977
, z	R. R. R. R. J. Ling, L. S. L., Moir, D. T.; King, B. L.; Brown, B. D.; Doig, P. C.; Smith, D. R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S. D.; Jiang, Q.; Taylor, D. E.; Vovis, G.F.; 1
Na A	Nature 397, 176-180, 1999 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathd
44	A;Reference number: A71800; MUID:99120557; PMID:9923682 A:Accession: B71977
44	A,Status: preliminary
Ä	A;Residue: 1-238 <arn></arn>
¥ 4	A;Cross-references: UNIPRCT:Q9ZMZ4; UNIPARC:UPI0000137D6F; GB:AE001446; GB:AE001439; NID: A:Rynerimental source: strain 199
ပြ	Cidentics:
A;	A,Gene: ureA
Ω.Ψ.(C;Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K c; F;1-101/Domain: urease 11K chain homology <u1.></u1.>
·.	F_i 108-204/Domain: urease 12K chain homology <012>
	3 2; Length 238; 5;
	Matches 119; Conservative 42; Mismatches 62; Indels 1; Gaps 1;
λō	-
ą	1 MKLTPKELDKLMLHYAGELARKRKEKGIKLNYVEAVALISAHIMEEARAGKKTAAELMOE 60
λõ	61 CMHFLKKDEVMPGVGNMVPDLGVEATPPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
qu	61
ò	
ΩD	: : :: :: :
ò	181 OTRKVQLIPLG
q	: : : :

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F;1-101/Domain: urease 11K chain homology <U11>F;108-204/Domain: urease 12K chain homology <U12>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complex: heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S35290
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                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: ureA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
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Infect. Immun. 60, 5259-5266, 1992
i, Title: Purification and characterization of the urease enzymes of Helicobacter species
i, Reference number: A49215; MUID:93084378; PMID:1452359
R;Labigne, A.; Cussac, V.; Courcoux, P.
Labigne, A.; Cussac, V.; Courcoux, P.
Lacteriol. 137, 1920-1931, 1991
A;Title: Shutile cloning and nucleotide sequences of Helicobacter pylori genes responsib A;Reference number: A38537; MUID:91161505; PMID:2001995
                                                                                                                                                                                                                                   A;Cross-references: UNIPROT: P14916; UNIPARC: UP1000002C3CD; GB:M60398; NID: 9149007; PIDN: R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Broodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-36,'R',38-48,'R',50-131,'PP',134-238 <CLA>
A; Cross-references: UNIPARC:UP100002DB17; EMBL:X17079; NID:g43633; PIDN:CAA34932.1; PID
R; Dunn, B.E; Campbell, G.P.; Perez-Perez, G.I.; Blaser, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Experimental source: strain UMAB41; Evans Jr., D.J.; Evans Jr., D.J.; Evans, D.Y. (icrob. Pathog. 10, 15-26, 1991; Trkpatrick, S.S.; Graham, D.Y. (icrob. Pathog. 10, 15-26, 1991; Tritle: Characterization of the Helicobacter pylori urease and purification of its subuly Reference number: A61371; MUID:91312104; PMID:1857197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and tw
C,Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-238 <TOM>
A;Cross-references: UNIPARC:UPI000002C3CD; GB:AE000529; GB:AE000511; NID:g2313152; PIDN:
A;Experimental source: strain 26695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cläyton, C.L.; Pallen, M.J.; Kleanthous, H.; Wren, B.W.; Tabaqchali, S.
Nucleic Acids Res. 18, 362, 1990
A.Title: Nucleotide sequence of two genes from Helicobacter pylori encoding for urease
A;Reference number: S07884; MUID:90221820; PMID:2326167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UP10000030924
R;Hu, L,T.; Mobley, H.L.T.
Infect. Immun. 58, 992-998, 1990
A;Title: Purification and N-terminal analysis of urease from Helicobacter pylori.
A;Reference number: A41502; MUID:90202165; PMID:2318539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 265, 9464-9469, 1990
A/Title: Purification and characterization of urease from Helicobacter pylori.
A/Reference number: A35306, MUID:90264448; PMID:2188975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPARC:UPI00000B16E0; PIDN:AAB24359.1; PID:g260968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A64529 (Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: heterodimer; hydrolase; metalloprotein
F;1-238/Product: urease 26K chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: strain NCTC 11637
Note: sequence extracted from NCBI backbone (NCBIP:119486)
Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: protein
Residues: 1-5, R', 7-20, R', 22-30 <EVA>
Cross-references: UNIPARC:UP10000172DA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-13,'S',15-20 <HUA>
A;Cross-references: UNIPARC:UP10000172DA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-20 < DUN>
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Residues: 1-12 <TUR>
                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-238 <LAB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B35306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A41502
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;Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and two subperfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K ch;Keywords: heterodimer; hydrolase; metalloprotein 11-101/bomain: urease 11K chain homology 
1-101/bomain: urease 11K chain homology

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: Q08715; UNIPARC: UPI0000137D6C; EMBL: X69080; NID: 9396160; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: S35290
R;Ferrero, R.L.; Labigne, A.
Mol. Microbiol. 9, 323-333, 1993
A;Title: Cloning, expression and sequencing of Helicobacter felis urease genes.
A;Reference number: S35290; MUID:94018627; PMID:8412683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                             61 GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 INAGKEAISLKVKNKGDRPVQVGSHFHFFEVNKLLDFDRAKSFCKRLDIASGTAVRFEPG 179
                                                                                                                                                                                                                                                                                                                                                                                                                               LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urease (BC 3.5.1.5) 26K chain - Helicobacter felis
N'Alternate names: urease alpha chain
C:Species: Helicobacter felis
C:Species: 31-Dec-1993 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
                                                                                                                                                                                               1 MKLTPKELDKLMLHYAGRLABEALARGVKLNYTEAVALISGRVWEKARDGNKSVADLMOE
                                                                                                                                                         1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       urease, beta/gamma subunit - Deinococcus radiodurans (strain R1)
                    Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                       Indels
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48.4%; Score 572; DB 1;
Best Local Similarity 50.0%; Pred. No. 5.8e-14;
Matches 112; Conservative 43; Mismatches 68;
                                                           1.3e-15;
                    Score 616; DB 1;
52.2%; Score . 1.3e-152.7%; Pred. No. 1.3e-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fil-101/Domain: urease 11K chain homology <U11>Fil08-204/Domain: urease 12K chain homology <U12>
                                                    Best Local Similarity 52.78
Matches 118; Conservative
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A; Molecule type: protein
A;Residues: 591-637 < TA4-
A;Cross-references: UNIPARC: UP10000172DA0
A;Cross-references: UNIPARC: UP10000172DA0
C;Comment: Bach chain of the hexamer binds two nickel ions.
C;Comment: Bach chain of the hexamer binds two nickel ions.
C;Comment: bach chain of the hexamer binds two nickel actions in monology; urease 12K chain homology (U12-
F;1-10/Domain: urease 12K chain homology (U12-
F;1-10/Domain: urease 62K chain homology (U12-
F;274-823/Domain: urease 62K chain homology (U2-
F;274-823/Domain: urease 62K chain homology (U2-
F;274-825/Domain: urease 62K chain homology (U12-
F;274-825/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted
F;490,519,545/Binding site: nickel 1 (Lys, His) #status predicted
F;490,Flanding site: carbon dioxide (Lys) (covalent) (by urease activase) #status predicte
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Fille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CM--HPLKKDEVMPGVGNMVPDLGVBATFPDGTKLVTVNWPI--BPDEHFKA--GEV--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KF-----G---C-DKDIELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 ALKFDREKAYGKRLDIPSGNTLRIGAGQTRKVQLIPLGGSKKVIGMN----GLVN--NIA 207
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               R'Takishima, K.; Mamiya, G.
Protein Seq. Data Anal. 1, 103-106, 1987
A;Title: Location of the essential cysteine residue of jack bean urease.
A;Reference number: S03364; MUID:88190054; PMID:3447159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Indels
                                                                                                                                                                         K.; Masakuni, M.; Kayumi, T.; Ogawa,
9, 1987
                                                                                                               A;Residues: 1-246,'R',248-257,'P',259-268,'S',270-840 <TA2>
A;Cross-references: UNIPARC:UP10000172D9F
                                                                                                                                                A,Cross-references: UNIPARC:UPI0000172D9F
R,Mamiya, G.; Takishima, K.; Masakuni, M.; Kayumi, T.; Oga
J. Protein Chem. 6, 55-59, 1987
A,Title: Complete amino acid sequence of jack bean urease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
39.1%; Score 462; DB 1;
Best Local Similarity 41.4%; Pred. No. 1.5e-08;
Matches 110; Conservative 45; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 DERH----K---HKALDKAKSHGFIK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 1-246,'R',248-840 <TA3>
A,Cross-references: UNIPARC:UP10000172D9E
          A; Reference number: JT0001
                                                                                                                                                                                                                                                                                         Reference number: A60883
                                                                               A; Molecule type: protein
                                                                                                                                         Cross-references:
                                                                                                                                                                                                                                                                                                                          Accession: A60883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S03364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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C;Species: Deinococcus radiodurans
C;Species: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 06-Jan-2003
C;Accession: D7586
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamanthevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Note: this sequence has been revised in reference JC1396
R;Takishima, K.; Suga, T.; Mamiya, G.
Rur. J. Biochem. 175, 151-165, 1988
A;Title: The structure of jack bean urease. The complete amino acid sequence, limited pr A;Reference number: S01021; MUID:88296463; PMID:3402446
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-228 «WH1»
A;Cross-references: UNIPARC:UP10000D3CO5; GB:AE001863; GB:AE001825; NID:g6460670; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: DRA0319
A;Map position: 2
C;Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K
                                                                                                                                                                                                                                                  A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: D75586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CMHF----LKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFK-AGE--VKF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 LMSFGAAILTPDDVLDGVPELIHEIOVEGTFPDGTKLVTVHDP1RGAASRRVAGEYLLEG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCDKDIELNAGKEVTELEVTINEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Date: 28-Dec-1987 #sequence revision 30-Sep-1993 #text change 05-Oct-2004 (C.Dates 28-Dec-1987) #sequence revision 30-Sep-1993 #text change 05-Oct-2004 (C.Dacession: JC1396; S01021; JT0001; A60883; S03364; JS0642 R;Riddles, P.W.; Whan, V.; Blakeley, R.L.; Zerner, B. Gene 121, 399-400, 1992 A;Reference number: JC1396; MUID:93077062; PMID:1446838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI0000172D9E
R;Mamiya, G.; Takishima, K.; Masakuni, M.; Kayumi, T.; Ogawa, K.; Sekita,
Proc. Jpn. Acad. B Phys. Biol. Sci. 61, 395-398, 1985
A;Title: Complete amino acid sequence of jack bean urease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P07374; UNIPARC:UP10000137DA7; GB:M65260 R;Riddles, P.W.; Whan, V.; Blakeley, R.L.; Zerner, B. Gene 108, 265-267, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 TLRIGAGQTRKVQLIPLGGSKKVIGMNGLVNNIAD-ERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.3%; Score 511; DB 2; Length 22:
45.7%; Pred. No. 1e-11;
ive 46; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          urease (EC 3.5.1.5) - jack bean
N;Alternate names: urea amidohydrolase
C;Species: Canavalia ensiformis (jack bean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 1-246,'R',248-840 <TAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.3%
Best Local Similarity 45.7%
Matches 106; Conservative
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A; Residues: 1-840 <RID>
                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary A; Molecule type: DNA
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Wighternate names: urea amidohydrolase; urease chain A; urease gamma chain C;Species: Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Accession: A36138; 832938
R;Mulrooney, S.B.; Hausinger, R.P.
J. Bacteriol. 172, 5837-5843, 1990
A;Title: Sequence of the Klebsiella aerogenes urease genes and evidence for accessory pro A;Reference number: A36138; MUID:91008957; PMID:2211515
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-835 <MCD>
A;Cross-references: UNIPROT:000084; UNIPARC:UPI0000137DA9; EMBL:AL109820; PIDN:CABS2575.1
A;Experimental source: strain 972h-; cosmid c1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: UNIPROT: P18316; UNIPARC: UP100001103C0; GB:M36068; NID:g149335; PIDN: R; Collins, C.M.; Gutman, D.M.; Laman, H. Morb. Microbloil. 8, 187-189; 1993
Mol. Microbloil. 8, 187-189; 1993
A)Fittle: Identification of a nitrogen-regulated promoter controlling expression of Klebsi A; Reference number: S32937; MUID:93268094; PMID:8497192
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A;Residues: 1-66,'K',68-100 <COL>
A;Cross-references: UNIPARC:UP10000137D9A; EMBL:L07039; NID:g149330; PIDN:AAA25147.1; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: urease; urease 11K chain homology; urease 12K chain homology; urease 62K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMLGKRHVQPNVVHLLHEIMIEATFPDGTYLITIHDPICTTDGNLEHALYGSFLPTPSQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 NKALKFDREKAYGKRLDIPSGNTLRIGAGQTRKVQLIPLGGSKKVIGMNGLVNNIADERH 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                               urease (EC 3.5.1.5) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Dete: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 12-Jul-2004
C;Accession: T37339
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEECM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 HFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPI-EPD---EH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 -FKAGEVKF-----G----CDKDIEL--NAGKEVTELEVTNEGPKSLHVGSHFHFFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
   172 VRFGPGERVEVGLVPIGGARVAIGFAGLVDGPLDAPGAREEALRRAAACGYL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.9%; Score 412; DB 2; Best Local Similarity 37.4%; Pred. No. 1.1e-06; Matches 95; Conservative 39; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA__
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 KHKALDKAKSHGFI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 TREIVDNLMKQĞFM 252
                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z21755
A;Accession: T37939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SPDB:SPAC1952.11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-100 <MUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: urease
C; Keywords: hydrolase
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셤
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R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw Mor. Microbiol. 21, 77-96, 1996
A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S A;Reference number: Z20556; MUID:97000351; PMID:8843436
                                                                                                                                                                               A;Gene: F12B7.10
A;Map position: 1
C;Superfamily: urease; urease 11K chain homology; urease 12K chain homology; urease 62K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: ureAB
C;Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K
C;Keywords: hydrolase
                                                                                                                     A;Cross-references: UNIPARC:UP100000ABA6F; GB:AE005173; NID:g6382524; PIDN:AAF07806.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIE----PDEHFKAGEVKFGCD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDIELNAGKEVTELEVTNEG--PKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PDEH----FKAGEVKFGCDKDIELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LDKFPEVHEGVIIPGDMKYG-DGSIIINHGRKAVVLKVVNTGDRPVQVGSHYHFIEVNPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKFDREKAYGKRLDIPSGNTLRIGAGOTRKVQLIPLGGSKKVIGMNGLVNNIAD----- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPI-----E------ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDEARRGKKTVAQLMEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRLTPTERDRLLLFGAAELARARARGLRLNVPEATALIADTVCEAARDGAR-LAQAIER 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              urease (EC 3.5.1.5) beta/gamma chain - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 06-Jan-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VKLIPKEQEKFLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDEARRGKKTVAQLMEE
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A;Cross-references: UNIPARC:UP10000DACF4; EMBL:AL031124; PIDN:CAA19973.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRIGAGQTRKVQLIPLGGSKKVIGMNGLVNNIAD-ERHKHKALDKAKSHGFI 225
                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                                                                                                                                                     Query Match 36.2%; Score 427; DB 2; Length 838; Best Local Similarity 38.0%; Pred. No. 3e-07; Matches 100; Conservative 47; Mismatches 73; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.2%; Score 416; DB 2; Length 227; 40.5%; Pred. No. 3.7e-08; Live 46; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: T29055
A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ERH--KH-KALDKAKSHG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0...
Best Local Similarity 40.59
Watches 94; Conservative
                                                         A; Molecule type: DNA
A; Residues: 1-838 <STO>
A;Accession: A96699
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Molecule type: DNA
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A;Cross-references: UNIPROT:08XAG2; UNIPARC:UPI00000D5DF7; GB:AE005174; NID:g12513945; PJ
A;Experimental source: strain O157:H7, substrain EDL933
A;Accession: E85654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI0000D5DF7; GB:AE005174; NID:g12514462; PIDN:AAG55697.1; (
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: B90794
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama; K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; MUID:21156231; PMID:11258796
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8XAG2; UNIPARC:UPI00000D5DF7; GB:BA000007; PIDN:BAB34745.1;
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          urease gamma subunit [imported] - Escherichia coli (strain O157:H7, substrain RIMD C;Species: Escherichia coli
C;Spacies: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ή:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: ureA; ureA_2
C;Superfamily: urease, gamma subunit; urease 11K chain homology
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C;Superfamily: urease, gamma subunit; urease 11K chain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.0%; Score 283; DB 2; Length 10 llarity 57.0%; Pred. No. 0.00052; Conservative 20; Mismatches 22; Indels
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <STO>
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A;Molecule type: DNA
A;Residues: 1-100 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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A;Molecule type: DNA
A;Residues: 1-100 <COL>
A;Essidues: 1-100 <COL>
A;Cross-references: UNIPROT:P50043; UNIPARC:UPI0000137D9C; GB:Z83859; GB:AL123456; NID:GA;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                              A Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and two Schuperfamily: urease, gamma subbunit; urease 11K chain homology C;Keywords: heterotrimer; hydrolase; heterotrimer; hydrolase; heterotrimer; hydrolase; F:1-100/Domain: urease 11K chain homology <0.11>
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                                                                                                                                                                                                                                                                                                                                                Complex: trimer of heterotrimeric subunits consisting of 11K (gamma), 12K (beta), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable urease structural subunit A (gamma) [imported] - Escherichia coli (strain O157:
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #רמיד רביי
C;Accession: הפרחי מחברים
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Accession: H70664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
      submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A6597; PDB:1KRA
A;Contents: annotation; X-ray crystallography, 2.3 angstroms, residues 1-100
R;Jabri, E.; Carr, M.B.; Hausinger, R.P.; Karplus, P.A.
Science 268, 998-1004, 1995
A;Title: The crystal structure of ureas Ribebiella aerogenes.
A;Reference number: A56340; MUID:95273988; PMID:7754395
A;Contents: annotation; X-ray crystallography, 2.3 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable ureA protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 24.3%; Score 287; DB 1; Length 100; 1 Similarity 59.0%; Pred. No. 0.00037; 59; Conservative 18; Mismatches 22; Indels
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Best Local Similarity
Matches 59; Conserv
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completed: August 9, 2006, 21:29:40
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C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: Bacillus subtilis
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: B69729
R; Munst, F: Ogasawara, N; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Sammerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sakaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togmoni, A.; Tosato, V.; Uchiyama,
A;Authors: P.; Wilpat, A.; Yamamoto, H.; Yasumoto, K.; Yata, K.; Yoshida, K.;
A;Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P73796; UNIPARC:UP10000137DA2; EMBL:D90909; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT:P75030; UNIPARC:UPI000060B96; GB:Z99122; GB:AL009126; NID:g
Experimental source: strain 168
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74889
E;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okmura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Accession: S74889
A;Status: nucleic acid sequence not shown; translation not shown
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58.0%; Pred. No. 0.00057;
iive 19; Mismatches 22; Indels
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F;1-100/Domain: urease 11K chain homology <U11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subunit; urease 11K chain hömology
metalloprotein
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55.8%; Pred. No. 0.00075;
tive 15; Mismatches 25.
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                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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C;Accession: A36950
R;Maeda, M; Hidaka, M.; Nakamura, A.; Masaki, H.; Uozumi, T.
J. Bacteriol. 176, 432-442, 1994
A;Title: Cloning, sequencing, and expression of thermophilic Bacillus sp. strain TB-90 un A;Reference number: A36950; MUID:94117379; PMID:8288539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q07399; UNIPARC:UPI0000137D95; GB:D14439; NID:g393296; PIDN:E
C;Superfamily: urease, gamma subunit; urease 11K chain homology
C;Keywords: hydrolase
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1 MKLTPVEQEKLLIFAAGELAKQRKARGVLLNYPEAAAYITCFIMEGARDG-KGVAELMEA 59
                                                                                                                                                                                                                                                                                           C;Species: Bacillus sp.
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
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55.0%; Pred. No. 0.00095;
tive 19; Mismatches 25.
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Best Local Similarity 55.0%
Matches 55; Conservative
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A;Molecule type: DNA
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1 VKLTPKEQEKFLLYYAGEVA......ADERHKHKALDKAKSHGFIK 226
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P14916
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 4.0 , Gapext 1.0
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1: uniprot_sprot:*
2: uniprot_trembl:*
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32 505 42.8 231 1 URE23 PSESSM 33 503 42.6 232 2 COSFB24 CAML. 34 502 42.5 231 2 COSFB24 CAML. 35 602 42.6 231 2 COSFB24 CAML. 35 602 42.6 231 2 COSFB24 CAML. 37 62 39.1 840 1 URA. CAMB. 39 448 37.8 172 2 GOSTGA HELLH 41 446 37.8 172 2 GOSTGA HELLH 42 446 37.8 172 2 GOSTGA HELLH 43 37.1 195 2 GOSTGA HELLH 44 43 37.5 185 2 COSFB3 HELLH 43 37.2 164 2 COSFB3 HELLH 43 37.2 164 2 COSFB3 HELLH 11 URA. HELLH 53 37.0 190 2 GOSTGA HELLH 44 33 77.2 164 2 COSFB3 HELLH 12 URA. HELLH 53 37.0 190 2 GOSTGA HELLH 44 33 77.5 186 2 COSFB3 HELLH 12 URA. HELLH 54 37.2 164 2 COSFB3 HELLH 54 43 37.2 164 2 COSFB3 HELLH 12 URA. HELLH 54 37.2 164 2 COSFB3 HELLH 54 43 37.2 164 2 COSFB3 HELLH 12 URA. HELLH 54 37.2 164 2 COSFB3 HELLH 54 43 37.2 164 2 COSFB3 HELLH 54 500 5 SEQUENCE OF S	URE23 PSESM Q883f3 pseudomonas OSFB24 CAMLA Q5fb24 campylobact Q4zU1 PSEU2 Q4zU1 pseudomonas Q35P06 PSEU2 Q35P06 PSEU2 Q35P06 PSEU2 Q35P06 PSEU3 Q35P06 PSEU3 Q37AC5 SOYBN PO7374 canavalia e Q8KTJ5 HELHE Q8KTJ9 HELHE Q8KTJ9 HELHE Q8KTJ9 HELHE Q8KTJ9 helicobacte Q8KTJ1 HELHE Q8KTJ9 helicobacte Q8KRJ4 HELHP Q9KZ1 HELHE Q9FBZ HELHP Q6FG C6FG CAMPA Q6FG HELED Q6FG CAMPA	ALIGNMENTS PRT; 234 AA. Ito UniProtKB/Swiss-Prot. 3.5.1.5) (Urea amidohydrolase alpha subunit). Epsilonproteobacteria; Campylobacterales; acter. In 20. Epsilonproteobacteria; Campylobacterales; acter. Chang Y.F.; Chang Y.F.; Chang Y.F.; Chang Y.F.; Chang Y.F.; Ion of a Helicobacter bizzozeronii urease gamma apha subunit and a beta subunit (By Cytoplasm (By similarity)) erminal section; belongs to the urease gamma erminal section; belongs to the urease gamma cerminal section; belongs to the urease beta erminal section; belongs to Learning to the urease beta erminal section; belongs to Learning to the urease beta erminal section; belongs to Learning to the urease beta erminal section; belongs to Learning to the urease beta erminal section; belongs to Learning to the urease beta erminal section; belongs to the urease beta erminal section; belongs to the urease license ergamma reg. Cytoplasm (By similarity) Ferial Samma reg. Epsilonproteobacteria; What is known, in belongs and the subunit. Ferial Epsilonproteobaction. Ferial I. Ferial Epsilonproteobacteria; I.	
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Urease gamma.
Urease beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenomeReviews, AE001439_GR, JHP0068.
BioCyc; HPYL85963:JHP0066-MONOMER; -
HAMAP; MF 00739; fused; 1.
InterPro; IPR002019; Urease beta.
InterPro; IPR002026; Urease_gamma_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                  1 102 ÜJ
103 234 ÜJ
234 AA; 25746 MW;
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HSSP; P14916; 1E9Z.
SMR; Q9ZMZ4; 1-238.
                                                                                                           Similarity
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                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infect. Immin. 62:1631-1638(1994).
-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- SUBCUIT: Heterodimer of an alpha subunit and a beta subunit.
-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
-!- SIMILARITY: In the N-terminal section; belongs to the urease gamma subunit family.
-!- SIMILARITY: In the C-terminal section; belongs to the urease beta subunit family.
-!- CAUTION: In Helicobacter the alpha subunit is what is known, in other bacteria as the beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solnick J.V., O'Rourke J., Lee A., Tompkins L.S.; "Molecular analysis of urease genes from a newly identified uncultured species of Helicobacter.";
                                                                                                           1 VKLITPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2006, entry version 35.
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase alpha subunit)
                                                                         6; Gaps
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Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                 GAGQTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                       Length 234;
                                 tch 56.3%; Score 665; DB 1; Length 23 sal Similarity 57.3%; Pred. No. 1.9e-17; 130; Conservative 39; Mismatches 52; Indels
 4567707785648843 CRC64;
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HSSP; P14916; 1E9Z.
SMR; P42822; 1-224.
HAMAP; MF_00739; fused; 1.
InterPro; IPR002019; Urease_gamma_reg.
InterPro; IPR002019; Urease_gamma_reg.
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Pfam; PF00547; Urease gamma; 1.
Pfam; PF00547; Urease gammabeta; 1.
ProDom; PD002326; Urease beta; 1.
ProDom; PD002319; Urease beta; 1.
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TIGRFAMS; TIGR00193; urease_gam; 1.
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MEDLINE=94222523; PubMed=8168924;
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 25720 MW;
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                                                  Local Similarity
234 AA;
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P428<u>2</u>2;
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Distributed under the Creative Commons Attribution-NoDerivs License
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-!-SUBCELULAR LOCATION: Cytoplasm (By similarity).
-!-SUBCELULARITY: In the N-terminal section; belongs to the urease gamma subunit family.
-!-SIMILARITY: In the C-terminal section; belongs to the urease beta subunit family.
-!-CAUTION: In Helicobacter the alpha subunit is what is known, in other bacteria as the beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                          61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEP-DEHFKAGEV--KFGCDK
                                                                                                                                                                                                                                     1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999, sequence version 1.
07-MAR-2006, entry version 37.
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase alpha subunit)
Name-ureA; Synonyms-hpuA; OrderedLocusNames-JHP0068;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                         Gaps
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Nature 397:176-180(1999)
-1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GAGQTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAK-SH-GFI 225
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                                                                        54.0%; Score 638; DB 1; Length 234; 54.8%; Pred. No. 2.2e-16;
                                                                                                                                                         Indels
CD5889E3D789C7F8 CRC64;
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EMBL; AF479027; AAL86897.1; -; Genomic_DNA
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MEDLINE=23001021; PubMed=14638992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q93NJ1 HELPY PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20123532; PubMed=10660136;
Opazo P., Muller I., Rollan A., Valenzuela P., Yudelevich A.,
Garcia-de la Guarda R., Urra S., Venegas A.;
"Serological response to Helicobacter pylori recombinant antigens in Chilean infected patients with duodenal ulcer, non-ulcer dyspepsia and
                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CH-CTXI;
MEDLINE=22121498; PubMed=12125208;
Muller I., Medina-Selby A., Palacios J.L., Martinez P., Opazo P.,
Muller I., Medina-Selby A., Palacios J.L., Martinez P., Opazo P.,
Eloning and comparison of ten gene sequences of a Chilean H. pylori
strain with other H. pylori strains revealed higher variability for
Biol. Res. 35:67-84 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                           DB 1; Length 238;
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                                                                                                                                                                                                            26568 MW; A10B9DC4156C0561 CRC64;
                                                                                                                                                            /FTId=PRO_0000098074.
Urease gamma.
Urease beta.
                                                                                                                                             Urease alpha subunit
                                                                                                                                                                                                                                                          Pred. No. 1.2e-15;
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01-JUN-2002, sequence version 1.
07-FEB-2006, entry version 19.
Urease A subunit.
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                                                                                                                                                                                                                                                     53.1%; Pred. ...
rive 42; Mismatches
           Pfam; PF00659; Urease Deta; 1.
Pfam; PF00547; Urease Gamma; 1.
Probom; PD002326; Urease Gammabeta; 1.
Probom; PD002319; Urease Deta; 1.
TIGRFAMs; TIGR00192; urease Deta; 1.
TIGRFAMs; TIGR00193; urease Deta; 1.
Complete proteome; Hydrolase.
CHAIN
                                                                                                                                                                                                                                           52.4%; Score 619;
InterPro; IPR008223; Urease_gammabeta
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                                                                                                                                                                                                                                                                         Matches 119; Conservative
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                            238 AA;
                                                                                                                                                                                                                                                          Local Similarity
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.2%; Score 617; DB 2; Length 238; 52.7%; Pred. No. 1.5e-15; ive 43; Mismatches 62; Indels
HSSP; P14916; 189Y.

SMR; QRNU5; 1-238.

R GO; GO: 00105137; C: Cytoplasm; IEA.

R GO; GO: 00105137; F: F: Cytoplasm; IEA.

R GO; GO: 00105137; F: F: Cytoplasm; IEA.

R GO; GO: 00005139; F: Rease activity; IEA.

R GO; GO: 0006807; P: nitrogen compound metabolism; IEA.

R GO; GO: 0006807; P: nitrogen compound metabolism; IEA.

R GO; GO: 0006807; P: nitrogen compound metabolism; IEA.

R InterPro; IPR002026; Urease_gamma_req.

InterPro; IPR00823; Urease_gamma_beta.

R Pfam; PF00699; Urease_pamma_beta.

R Pfam; PF00699; Urease_beta; 1.

R ProDom; PD002135; Urease_gamma. 1.

R ProDom; PD002195; Urease_gamma. 1.

R TIGRFAMS; TIGR00193; urease_gamma. 1.

R TIGRFAMS; TIGR00193; urease_gamm; 1.

R TIGRFAMS; TIGR00193; urease_gam; 1.

SEQUENCE 238 AA; 26710 MW; R934A6512A559B28 CRC64;
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GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0016807; F:nitrogen compound metabolism; IEA.
InterPro; IPR002019; Urease_beta.
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01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 20.
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Microbiol, Immunol. 47:813-821(2003).
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"Shuttle cloning and mucleotide sequences of Helicobacter pylori genes responsible for urease activity.";
J. Bacteriol. 173:1920-1931(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992, sequence version 2.
07-MAR-2006, entry version 57.
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase alpha subunit)
Name-ureA; Synonyms-hpuA; OrderedLocusNames-HP0073;
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MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

Tomb J.-F., White O., Kerlavage A.R., Clayron R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.
Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
Kelley J.M., Cotton M.D., Weidman J.F., Fulji C., Bowman C.,
Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90221820; PubMed=2326167;
Clayton C.L., Pallen M.J., Kleanthous H., Wren B.W., Tabaqchali S.;
"Nucleotide sequence of two genes from Helicobacter pylori encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                             Length 238;
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53.1%; Pred. No. 1.5e-15;
iive 43; Mismatches 61; Indels
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InterPro; IPR002026; Urease_gamma_reg.
InterPro; IPR008223; Urease_gammabeta.
Pfam; PR00699; Urease_beta; 1.
Pfam; PR00547; Urease_gammabeta; 1.
PINSF; PINSF001225; Urease_gammabeta; 1.
ProDom; PD002326; Urease_beta; 1.
ProDom; PD002319; Urease_beta; 1.
TIGRPAMS; TIGR00103; urease_beta; 1.
TIGRPAMS; TIGR001093; urease_gam; 1.
SEQUENCE 238 AA; 26672 NW; EE822BF961D03
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MEDLINE=91161505; PubMed=2001995;
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.1<sup>3</sup>
Matches 119, Conservative
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ID UREA_HELPY
AC P14916;
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Distributed under the Creative Commons Attribution-NoDerivs License
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-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).

-!- SUBUNIT: Heterohexamer of 3 alpha and 3 beta subunits. Four heterohexamers assemble to form a 16 nm spherical complex.

-!- SUBCELLALAR LOCATION: Cytoplasm.

-!- MISCELLANEOUS: Oligomerization may protect the enzyme against denaturation in an acidic environment.

-!- SIMILARITY: In the N-terminal section; belongs to the urease gamma subunit family.

-!- SIMILARITY: In the C-terminal section; belongs to the urease beta
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-!- CAUTION: In Helicobacter the alpha subunit is what is known, in other bacteria as the beta subunit.
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                                                                                                                                                                                                                                                                                                                                                                                               Akada J.K., Shirai M., Takeuchi H., Tsuda M., Nakazawa T.;
"The urease operon in Helicobacter pylori is regulated by decay of
Smith H.O., Fraser C.M., Venter J.C.; "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 1-20.

PROTEIN SEQUENCE OF 1-20.

HU L.T., Mobley H.L.T.;

"Purification and N-terminal analysis of urease from Helicobacter

"Purification and N-terminal analysis of urease from Ferminal Analysis of Urease From
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn B.E., Campbell G.P., Perez-Perez G.I., Blaser M.J.; "Purification and characterization of urease from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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EMBL, M60398; AAA25020.1; -; Genomic_DNA.
EMBL, A08816; CAA00810.1; -; Unassigned DNA.
EMBL, A07396; CAA01662.1; -; Unassigned_DNA.
EMBL, AB00511; AAB07144.1; -; Genomic_DNA.
EMBL, AB032429; BAA84532.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 1-20.
MEDLINE=90264448; PubMed=2188975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infect. Immun. 58:992-998(1990).
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PDB; 1E9Z; X-ray; A=1-238.
                                                                                                                                                                       Nature 388:539-547(1997)
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PDB; 1E9Y; X-ray; A=
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF373570; AAK69736.1; -; Genomic_DNA.
R18SP; P14916; IBSY.
SWR; Q93N13; 1-238.
R GO; GO: 0005737; C: Cytoplasm; IEA.
GO; GO: 00016151; F: F: F: Civit ion binding; IEA.
GO; GO: 0008039; F: Urease activity; IEA.
R GO; GO: 00080039; F: P: F: Civit ion binding; IEA.
R GO; GO: 00080039; F: P: Civit ion binding; IEA.
R GO; GO: 00080039; F: Civit ion binding; IEA.
R GO; GO: 00080039; F: Civit ion binding; IEA.
R GO; GO: 00080039; F: Civit ion binding; IEA.
R GO; GO: 000800309; F: Civit ion binding; IEA.
R FAPTOPO; IPRO02026; Urease_GammaDeta.
R PFODSA; Tivit ion compound metabolism; IEA.
R PFODOM; PD002125; Urease_Deta; 1.
R PFODOM; PD002125; Urease_Deta; 1.
R PFODOM; PD00219; Urease_Deta; 1.
R TIGREAMS; TIGREO0193; urease_Deta; 1.
TIGREAMS; TIGREO0193; urease_Deta; 1.
R TIGREAMS; TIGREO0193; urease_Gam; 1.
R TIGREAMS; TIGREO0193; urease_Gam; 1.
R SEQUENCE 238 AA; 26587 WW; DFDBA17D016FC351 CRC64;
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                                                                         : : |:|| :|||::| | || || || EEKSVELIDIGGSRRIFGFNALVDRQADNESKKIALHRAKERGF
                                                                                                                                                                                                                                                                                    01-DEC-2001, integrated into UniProtKB/TrEMBL. 01-DEC-2001, sequence version 1. 07-FBB-2006, entry version 20. Urease protein UreA.
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MEDLINE=23001021; PubMed=14638992;
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    Urease gamma.
Urease beta.
H -> S (in Ref. 6).
A -> R (in Ref. 2).
A -> R (in Ref. 2).
KN -> PP (in Ref. 2).
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; Pred. No. 1.6e-15;
43; Mismatches 62;
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al Similarity 52.7%;
118; Conservative 4
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Best Local S
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STRAIN=34K, and 8K;
                                                                        NUCLEOTIDE SEQUENCE
                                                NCBI_TaxID=210;
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                         Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                            Chu C., Yu Y.J., Kong M.S., Ou J.T.; "Rate of Helicobacter pylori infection in children and clonality of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.2%; Score 616; DB 2; Length 238; 52.7%; Pred. No. 1.6e-15; Live 43; Mismatches 62; Indel8
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                                                                                                                                                                                                                                                                                                                                            GG; GG:0005737; C:cytoplasm; IEA.
GG; GG:0005737; C:cytoplasm; IEA.
GG; GG:0005033; F:urckel ion binding; IEA.
GG; GG:0009033; F:urcase activity; IEB.
GG; GG:0006037; F:urcase beta.
InterPro; IPR002019; Urcase_beta.
InterPro; IPR008223; Urcase_gamma_reg.
InterPro; IPR008223; Urcase_gamma_beta.
Ffam; PF00699; Urcase_gamma.
Ffam; PF00699; Urcase_gamma.
Froncm; PF00547; Urcase_gamma.
R ProDom; P002126; Urcase_beta; I.
R ProDom; P002119; Urcase_gamma.
R TIGRFAMS; TIGR00193; urcase_beta; I.
R TIGRPAMS; TIGR00193; urcase_beta; I.
SEQUENCE 238 AA; 26540 MW; 251AD890042A4262 CRC64;
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Q93NIB HELPY
ID Q93NIB HELPY
AC Q93NIB,
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Urease protein UreA.
                    Q33NIS_HELPY PRELIMINARY; PRT; 238 AA. Q93NIS.
01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 20.
Urease protein UreA.
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HSSP; P14916; 1E9Y.
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Microbiol. Immunol. 47:813-821(2003)
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STRAIN=47;
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                                                                                                                                             NCBI_TaxID=210;
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61 CMHFLKKOEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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Helicobačter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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GG; GG:0005737; C:cytoplasm; IEA.
GG; GG:0005039; F:uicase cativity; IEA.
GG; GG:0006003; F:uitzogen compound metabolism; IEA.
GG; GG:0006007; F:uitzogen compound metabolism; IEA.
InterPro; IPR002019; Urease_beta.
InterPro; IPR002025; Urease_gammabeta.
R InterPro; IPRS001225; Urease_gammabeta.
R Ffam; PP00699; Urease_beta; 1.
R PERSF; PIRSF001225; Urease_gammabeta; 1.
R PTODOm; PD002319; Urease_gammabeta; 1.
R PTODOm; PD002319; Urease_gammabeta; 1.
R TIGRFAMS; TIGR00192; urease_beta; 1.
R TIGRFAMS; TIGR00193; urease_beta; 1.
R TIGRFAMS; TIGR00193; urease_gamm; 1.
R TIGRFAMS; TIGR00193; urease_gam; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.1%; Score 615; DB 2; 52.7%; Pred. No. 1.8e-15; ive 43; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 20.
Urease protein UreA.
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HSSP; P14916; 1E9Y.
SWR; Q93N18; 1-238.
                                                                                                                                                                                                                                                                                                                Taiwan strains.";
Microbiol. Immunol. 47:813-821(2003)
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                                                                                                                                                                                          STRAIN=46;
MEDLINE=23001021; PubMed=14638992;
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Q933M9;
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Matches 118; Conservative
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MEDLINE=23001021; PubMed=14638992;
              EMBL; AF373584; AAK69750.1;
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Matches 118; Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=23001021; PubMed=14638992;
Chu C., Yu Y.J., Kong M.S., Ou J.T.;
"Rate of Helicobacter pylori infection in children and clonality of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WUCLECTIDE SEQUENCE.
STRAIN=100, 101, 5c, 85K, 86K, and 89k;
MEDLINE=23001021; PubMed=14638992;
MEDLINE=23001021; Kong M.S., Ou J.T.;
"Rate of Helicobacter pylori infection in children and clonality of Taiwan strains.";
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Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                 52.0%; Score 614; DB 2; Length 238; 52.7%; Pred. No. 2e-15; ive 43; Mismatches 62; Indels
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ProDom; PD002326; Urease_beta; 1.
ProDom; PD002319; Urease_gamma; 1.
TIGRFAMS; TIGR00192; Urease_beta; 1.
TIGRFAMS; TIGR00193; Urease_gam; 1.
SEQUENCE 238 AA; 26600 MW; 64A0C32A043A88D8 CRC64;
                                                                                                                                                    GO, GO:0005737; C:cytoplasm; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0006807; F:nitrogen compound metabolism; IEA.
InterPro; IPR002019; Urease_beta.
InterPro; IPR002026; Urease_gamma_reg.
InterPro; IPR008233; Urease_gamma_beta.
Pfam; PR00699; Urease_beta; 1.
Pfam; PR00547; Urease_gamma_beta.
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01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 21.
Urease protein UreA.
                                                                                                                EMBL; AF373580; AAK69746.1; -; Genomic_DNA.
EMBL; AF373572; AAK69738.1; -; Genomic_DNA.
HSSP; P14916; 1E9Y.
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                                        Taiwan strains.";
Microbiol. Immunol. 47:813-821(2003).
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Matches 118; Conservative
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61 CMHPLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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Distributed under the Creative Commons Attribution.NoDerivs License
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 238;
                                                                                                                                                                                                                 GO; GO: 0005737; C: Cytoplasm; IEA.
GO; GO: 0005737; C: Cytoplasm; IEA.
GO; GO: 0005039; F: Unickel ion binding; IEA.
GO; GO: 0006807; F: Unitrogen compound metabolism; IEA.
InterPro; IPR002035; Urease_beta.
InterPro; IPR002035; Urease_gamma_reg.
InterPro; IPR008023; Urease_gamma_beta.
Ffam; PF00699; Urease_beta; I.
Pfam; PF00699; Urease_gammabeta.
PIRSF; PIRSF001225; Urease_gammabeta; I.
ProDom; PD002316; Urease_beta; I.
ProDom; PD002319; Urease_beta; I.
TIGRFAMS; TIGR00192; urease_beta; I.
TIGRFAMS; TIGR00193; urease_gamma; I.
TIGRFAMS; TIGR00193; urease_gam; I.
SEQUENCE 238 AA; 26614 MW; E4A2917D016FD8DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%; Score 613; DB 2; Length 23 52.7%; Pred. No. 2.1e-15; ive 43; Mismatches 62; Indels
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                EMBL, AP373559; AAK69723.1; -; Genomic_DNA.
EMBL, AP373561; AAK69725.1; -; Genomic_DNA.
EMBL, AP373561; AAK69747.1; -; Genomic_DNA.
EMBL, AP373582; AAK69748.1; -; Genomic_DNA.
EMBL, AP373583; AAK69749.1; -; Genomic_DNA.
HSSP; P14916; 1E9Y.
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HSSP; P14916; 1E9Y.
SMR; Q93N14; 1-238.
Genomic_DNA
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Name=ureA;
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                             51.9%; Score 613; DB 2; Length 238; 52.2%; Pred. No. 2.1e-15; ive 44; Mismatches 62; Indels
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GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0009039; F:urease activity; IEA.
GO; GO:0006807; P:nitrogen compound metabolism; IEA.
InterPro; IPR002019; Urease_beta.
InterPro; IPR0020202; Urease_gamma_reg.
InterPro; IPR008203; Urease_gamma_reg.
PINTERPO; IPR006923; Urease_gamma_beta.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0009039; F:urease activity; IEA.
GO; GO:0006807; P:nitrogen compound metabolism; IEA.
INTERPY: IPR002019; Urease Deta.
InterPro; IPR008229; Urease_gamma_reg.
InterPro; IPR008229; Urease_gammabeta.
Pfam; PF00699; Urease_gammabeta.
Pfam; PF00699; Urease_gammabeta.
Pfam; PF00699; Urease_gammabeta.
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HSSP; P14916; 1E9Y.
SWR; Q93NJO; 1-238.
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Q93NJO;
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MEDLINE=23001021; PubMed=14638992;
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61 GRTLLKPDDVMDGVASMIHEVGIBAMFPDGTKLVTVHTPIBANGKLVPGEL-FLKNEDIT 119
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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GO; GO: 0005737; C: Cytoplasm; IEA.

GO; GO: 0005039; F: Utrease extivity; IEA.

GO; GO: 00068039; F: Utrease extivity; IEA.

GO; GO: 0006803; F: Utrease gamma reg.

InterPro; IPR002035; Urease_gammabeta.

InterPro; IPR002035; Urease_gammabeta.

Ffam; PP0059; Urease_gammabeta.

Pfam; PP0059; Urease_gammabeta.

Pfam; PP00547; Urease_gammabeta.

PTGRP; PIRSF001225; Urease_gammabeta; 1.

ProDom; PD002336; Urease_gammabeta; 1.

PTGRPMB; TIGR00193; Urease_gamma; 1.

TIGRPAMB; TIGR00193; Urease_gamma; 1.

TIGRPAMB; TIGR00193; Urease_gamm; 1.

SEQUENCE 238 AA; 26630 MW; E4A2917D17B5DBDB CRC64;
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                                                                                                                                                                                                                                                                                                         62; Indels
Pfam; PF00547; Urease_gamma; 1.
PIRSF; PIRSP001225; Urease_gammabeta; 1.
ProDom; PD002326; Urease_beta; 1.
ProDom; PD002319; Urease_gamma; 1.
PIGRPAMs; TIGR00192; urease_gam; 1.
TIGRPAMs; TIGR00193; urease_gam; 1.
SEQUENCE 238 AA; 26630 MW; 5C082660AAC88469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.9%; Score 613; DB 2;
52.7%; Pred. No. 2.1e-15;
iive 43; Mismatches 62.
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01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 20.
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HSSP; P14916; 1E9Y.
SMR; Q93NJ2; 1-238.
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Microbiol. Immunol. 47:813-821(2003)
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MEDLINE=23001021; PubMed=14638992;
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Best Local Similarity 52.7%
Matches 118; Conservative
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                                                                                                                                                                                                         61 CMHFLKKDEVMPGVGNMVPDLGVEATPPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                             121 INAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
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                                                                                                                                     1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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     Length 238;
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51.9%; Score 613; DB 2; Length 23 52.7%; Pred. No. 2.1e-15; ive 43; Mismatches 62; Indels
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Karimi Arzenani M., Mohammadi M.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0016787; P:hydrolase activity; IEA.
GO; GO:0016151; P:nickel ion binding; IEA.
GO; GO:0009039; P:urease activity; IEA.
GO; GO:0009039; P:urease activity; IEA.
GO; GO:0006807; P:nitrogen compound metabolism; IEA.
InterPro; IPR002019; Urease_Deta.
InterPro; IPR008225; Urease_Gamma reg.
InterPro; IPR008225; Urease_Gammabeta.
PEam; PF00547; Urease_Bamma; 1.
Pfam; PF00547; Urease_Gammabeta; 1.
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OH-UNA-2003, integrated into UniprotKB/TrEMBL. 01-JUN-2003, sequence version 1. 07-FRB-2006, entry version 15. Urease alpha (BC 3.5.1.5).
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HSSP; P14916; 1E9Y.
SMR; Q84F76; 1-238.
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Probom; PD002319; Urease_gamma; 1.
TIGRFAMs; TIGR00192; urease_beta; 1.
TIGRFAMs; TIGR00193; urease_gam; 1.
  Query Match 51.9
Best Local Similarity 52.7
Matches 118; Conservative
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Matches 118; Conservative
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120

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Db 61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119

Qy 121 LANGKEVTELEVTNEGPRSLHVGSHFHFPEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180

120 INEGKKAVSVKVKNVGDRPVQVGSHLHFPEVNRCLDFDREKTFGKRLDIASGTAVRFEPG 179

Qy 181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224

180 GRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 223

Search completed: August 9, 2006, 21:28:55

Job time : 302 secs
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GenCore version 5.1.9
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9, 2006, 21:34:02; Search time 196 Seconds August

Run on:

(without alignments) 1324.995 Million cell updates/sec

US-09-904-994B-3 Title: Perfect score:

1 MKMKKQEYVNTYGPTKGDKV......KLCTSKPTSQVPLAQRYTFF Sequence:

268

BLOSUM62 Scoring table:

2589679 seqs, 457216429 residues Gapop 4.0 , Gapext 1.0 Searched:

2589679 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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6: geneseqp2003as:*
7: geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

SUMMARIES

Description	Adj58239 Urease su	Adj58251 UreaseXY	Adj58242 UreaseXY	Adj58248 UreaseXY	Adj58245 UreaseXY	Adq37851 H. bizzoz	Aar04580 Part of p	Aaw07194 H. pylori	Aaw98511 H. pylori	Abu30687 Protein e	Adu05536 H. pylori	Ads09177 H. pylori	Aeb55116 Hylicobac	Aar67378 H. pylori	Aar74337 Helicobac	Aaw06730 H. felis	Aaw80599 Helicobac	Aar67371 Urease A	Aar13550 B subunit	Adm28644 Helicobac	Aar36387 Urease ga	Abul9714 Protein e	Abu41362 Protein e
ΩΙ	ADJ58239	ADJ58251	ADJ58242	ADJ58248	ADJ58245	ADQ37851	AAR04580	AAW07194	AAW98511	ABU3 0 6 8 7	ADU05536	ADS09177	AEB55116	AAR67378	AAR74337	AAW06730	AAW80599	AAR67371	AAR13550	ADM28644	AAR36387	ABU19714	ABU41362
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Length	568	568	268	268	496	569	269	569	569	569	569	568	570	269	569	269	749	908	559	559	568	268	995
% Query Match	100.0	99.1	98.7	98.5	86.4	77.6	9.9/	9.9/	9.9/	9.91	9.9/	16.1	76.1	76.1	74.8	74.8	74.8	74.6	74.6	74.3	67.7	64.3	64.1
Score	2999	2973	2960	2953	2591	2326	2297	2297	2297	2297	2297	2282	2282	2281	2244	2244	2243	2238	2237	2229	2029	1927	1921
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Abu21842 Protein e	Abu22314 Protein e	Abu30286 Protein e	Abu38819 Protein e	Abo78141 Pseudomon	Abu32083 Protein e	Adf05744 Bacterial	Abu41210 Protein e	Abo62699 Klebsiell	Ada34625 Acinetoba	Aar67379 P. mirabi	Abul7040 Protein e	Aaw37774 Klebsiell	Aay81825 Klebsiell	Abu28899 Protein e	Abu28920 Protein e	Adc00113 Enterohae	Abu40328 Protein e	Aar67380 Jack bean	Aag81512 S. epider	Abu42650 Protein e	Abp40181 Staphyloc
ABU21842	ABU22314	ABU30286	ABU38819	ABO78141	ABU32083	ADF05744	ABU41210	AB062699	ADA34625	AAR67379	ABU17040	AAW37774	AAY81825	ABU28899	ABU28920	ADC00113	ABU40328	AAR67380	AAG81512	ABU42650	ABP40181
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24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

immunogenic fragment; antibacterial; Vaccine; Helicobacter felis. ADJ58239 standard; protein; 568 AA. Urease subunit polypeptide Y. 11-JUL-2001; 2001EP-00202666. 17-JUL-2000; 2000EP-00202565. (first entry) Cattoli G; (ALKU) AKZO NOBEL NV. WPI; 2002-124384/17. N-PSDB; ADJ58237. Helicobacter felis BP1176192-A2 06-MAY-2004 30-JAN-2002. Kusters JG, ADJ58239; RESULT 1 ADJ58239

Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of vaccines.

Claim 10; SEQ ID NO 3; 76pp; English.

The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis in Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an urease Y subunit polypeptide of the invention.

Sequence 568 AA;

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                                      1 MKMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSP
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 Length 568;
                    Indels
ch 100.0%; Score 2999; DB 5; Il Similarity 100.0%; Pred. No. 3.3e-52; 568; Conservative 0; Mismatches 0;
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N-PSDB; ADJ58249.
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     Novel Helicobacter felis urease X and Y subunit polypeptides, useful i
the diagnosis of Helicobacter felis infections and in the preparation
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Pred. No. 1.1e-51;
4; Mismatches 2; Indels
                                                                                                                Disclosure; SEQ ID NO 15; 76pp; English.
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Best Local Similarity 98.9%;
Matches 562; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 568 AA;
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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis. Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an ureaseXY subunit of the invention.
                    481 HCKAKFDTSITFVSKVAYENGVKEKLGLERKVLPVKNCRNITKKDFKFNNKTAHITVDPK 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEAL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIRAABEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEY
Gaps
                                                                                                                                                                                                                                                                                                                                                           antibacterial; Vaccine; Helicobacter felis.
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                                                                               Disclosure; SEQ ID NO 12; 76pp; English
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                                                                                                                                                                                                  ADJ58248 standard; protein; 568
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Matches 558; Conservative
                                                                                                                                                                                                                                                                                                                                                           immunogenic fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALKU ) AKZO NOBEL NV
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                                                             541
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immunogenic fragment; antibacterial; Vaccine; Helicobacter felis.
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Pred. No. 2e-51;
4; Mismatches 4; Indels
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                                      Helicobacter felis
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                                                                             EP1176192-A2
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Zhu J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-2003; 2003US-00639273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGKAKFDTSITF-VS 494
99.2%;
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                   Matches 491; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibacterial; enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHAN/) CHANG Y.
(SIMP/) SIMPSON K W.
(ZHUJ/) ZHU J.
 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis. Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an ureaseXY subunit of the invention.
                PIIPYIINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDIGVIAMTSS 360
                                                                                                                                                                            HGKAKPDISITFVSKVAYENGVKEKGGERKVLPVKNCRNITKKDFKFNNKTAHITVDPK 540
                                                                                     PTIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSS 360
                                                                                                                                                          DSQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSE 420
                                                                                                                                                                                                                               YIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGH 480
                                                                                                                                                                                                                                                                                                  HGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPK 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogenic fragment; antibacterial; Vaccine; Helicobacter felis.
                                                                                                                                                                                                                                                                                                                                                                       TFEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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                                                                                                                                                                                                                                                                                                                                                                                          ADJ58245 standard; protein; 496 AA
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N-PSDB; ADJ58243.
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DB 5; Length 496;

86.4%; Score 2591;

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                                                                                                                                                                                                             121 AGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITFGKWNLHR
                                                                                                                                                                                                                                                                               181 MLRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEY
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                                                                                                                            DENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEAL
                                                                                                                                              61 DENTLDEVITNAMIDYTGIYKADIGIKNGKIHGIGKAGNKDMODGVSPHMVVGVGTEAL
                                                                                 1 MKMKKQEYVNTYGPTTGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSP
                                                                                                                                                                                            AGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHR
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                                                             1 MKMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSP
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                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urease; urease gene cluster; urease structural gene;
urease accessory gene; ureB; Helicobacter bizzozeronii infection;
                              ;
                              Indels
Pred. No. 4.3e-44;
                            1; Mismatches
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N-PSDB; ADQ37850.
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Novel isolated nucleic acid molecule having urease gene cluster, and conferring on Helicobacter bizzozeronii ability to produce urease, useful as vaccine for preventing disease in mammals infected by H.bizzozeronii.
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Claim 24; SEQ ID NO 5; 40pp; English

Helicobacter bizzozeronii an ability to produce urease, where the nucleic acid molecule is a urease gene cluster comprising at least one urease structural gene and at least one urease accessory gene. The nucleic acid molecule is chosen from urea, ureb, ureb, ured, ureh and urel. The nucleic acid, a vaccine for preventing onset of disease in mammals infected by H. bizzozeronii comprising a nucleic acid and a carrier, and an isolated by Edizozeronii comprising a nucleic acid and a carrier, and an isolated on nucleic acid, proteins and antibodies are useful for vaccinating mammals against onset of disease caused by infection of H. bizzozeronii, which involves administering the sequences. The sequences are useful for detecting H. bizzozeronii in a sample of tissue or body fluids which involves providing a nucleoic acid as an antigen, providing an antibody. Or providing a nucleotide sequence as a probe in a nucleic acid hybridisation assay, contacting the sample with the antigen or the probe, and detecting any reaction which indicates that H. bizzozeronii ureB prosent in the sample. This sequence represents the H. bizzozeronii ureB invention relates to an isolated nucleic acid molecule conferring

Sequence 569 AA;

ö 77.6%; Score 2326; DB 8; Length 569; 74.1%; Pred. No. 1.2e-38; ive 75; Mismatches 72; Indels C 420; Conservative Best Local Similarity Matches 420; Conserv Query Match

122 62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181 62 2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD S SHELDLVLTNALIVDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVCNNLCVGPATRALA d ò 셤 ð ઠ

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303 TIPPTVNTEAEHMDMLMVCHHLDKNIKEDVQFADSRIRPQTIAAEDKLHDMGIFSITSSD 362 363 SQAMGRVGEVITRIMQTADKNKKEFGRLPEEKGDNDNFRIKRYISKYTINPALAHGISEY SOAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY 362

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IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT 422

FEVFVDGKLCTSKPTSQVPLAQRYTFF 568

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See also New nucleotide sequences encoding Campylobacter pylori-ureaseents - and derived vectors, transformants, protein, antibodies and probes, useful in diagnosis, treatment and prevention of infections. The protein can be used for the prodn. of antibodies and to prepare vaccines for the prevention /treatment of C. pylori infections. See als AARA6578-81. (Updated on 25-MAR-2003 to correct PA field.) (Updated on -ocr-2003 to standardise OS field) (INSP) INST PASTEUR. (INRM) INSERM INST NAT SANTE & RECH MED Part of protein with urease activity Z Claim 12; Page 34; 47pp; French. AAR04580 standard; protein; 569 88FR-00013135. 88FR-00013135 (revised) (first entry) Helicobacter pylori WPI; 1990-147844/19. N-PSDB; AAQ04329 Sequence 569 AA; Urease; probe 06-OCT-1988; WO9004030-A. 24-OCT-2003 25-MAR-2003 21-SEP-1990 19-APR-1990 Labigne A; AAR04580; AAR04580

ö 242 61 62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 242 VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 2 KWKKQEYVNTYGPIKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD 182 LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD Gaps 0 Length 569; 75; Indels Query Match 76.6%; Score 2297; DB 2; Best Local Similarity 73.4%; Pred. No. 4.5e-38; Matches 416; Conservative 76; Mismatches 75; Query Match Best Local Similarity 122 g d ઠે ð a ò ò d ò

362 TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD

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New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and
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            243 VQVAIHTDTLNEAGCVEDTMAAIAGRIMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP
                                                                                                                                                                                                             LRAABEYSMINGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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                                                                                                                                                                                                 TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                                                                                                           422 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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543 YHVFVDGKEVTSKPANKVSLAQLFSIF
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97US-00902615
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24-JUN-1997;
29-JUL-1997;
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Vectors, e.g. pQRV314 (see also AAT44351), carrying the gene locus can be used to transform host cells for the large-scale prodn. of recombinant, enzymatically inactive, multimeric urease. The urease complex induces a mucosal immune response that can treat or prevent Helicobacter, esp. H. pylori, gastroduodenal infection. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine for inducing mucosal response to Helicobacter - contg. multimeric urease complex and pref. an antibiotic, anti-secretory agent or bismuth
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                                                                                                     | IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGWVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                           GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
SQAMGRAGEVI PRTWQTADKNKKEFGKLPEDGKDNDNPRIKRYISKYTINPALTHGVSEY
             SQAMGRVGEVITRTWQTADKONKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY
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Bhagat H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ackerman SK, Thomas WD,
, Ermak T, Guirakhoo F,
                                                                                                                                       FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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543 YHVFVDGKEVTSKPANKVSLAQLFSIF 569
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                                                                                                                                                                                                                                                                                                                             Urease; ureA gene; ureB gene; vaccine
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                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori; strain CPM630.
                                                                                                                                                                                                           AAW07194
ID AAW07194 standard; protein; 569
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95US-00568122
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                                                                                                                                                                                                                                                                     (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORAV-) ORAVAX INC.
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06-DEC-1995;
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Best Local S:
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                                                                                                                                                                                                                                   62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                        123 GEGLIVTAGGIDTHIHPISPQOIPTAFASGVTTMIGGGTGPADGTNATTITFGRRNLKWM 182
                                                                                                                                                                                                                                                                                                                                 183 IRAAEEYSMNIGFLAKGNASNDASLADQIEAGAIGFKIHEDWGTTPSAINHALDVADKYD 242
                                                                                                                                                                                                                                                                                                                                                                            243 VQVAIHTDTLNEAGCVEDTWAAIAGRTWHTFHTEGAGGHAPDIIKVAGEHNILPASTNP 302
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                                                                                                                                                                                                      This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastrits, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also bused for the production of antibodies. The products can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                             GEGMI ITAGGI DSHTHFLS PQQPPTALANGVTTMFGGGTGPVDGTNATTI TPGKWNLHRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 SQAMGRVGEVITRTWQTADKNXKEFGRLKEEKGDNDNFRIKRYLSKYTINPALAHGISEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KWKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                                                                                                                                                                                                                                                                                                       LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                                                                                                                VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTTP
                                                                                                                                                                                                                                                                                                                                                                                                           TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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                                                                                                                                                                      Gaps
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                                                                                                                                               76.6%; Score 2297; DB 2; Length 569; 73.4%; Pred. No. 4.5e-38; ive 76; Mismatches 75; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #16214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 YHVFVDGKEVTSKPANKVSLAQLFSIF 569
                     Claim 8; Page 960-962; 2054pp; English.
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gastrointestinal diseases.
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                                                                                                                                                           Best Local Similarity ... Matches 416; Conservative
                                                                                                                                                          Similarity
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Best Local 8
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proince operably linked to the nucleic acid nucleic acid; (2) a host cell containing the vector; (3) an isolated of encoding a polypeptide whose expression is inhibited by the antisense contined acid; (4) an antibody capable of specifically binding captisense nucleic acid; (4) an antibody capable of specifically binding captisense nucleic acid; (4) an antibody capable of specifically binding captisense nucleic acid; (4) an antibody capable of specifically binding contined proliferation or the activity of agene in an operon required for proliferation or the activity of agene in an operon required for captised fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENTLDLVI TNAMI I DYTGI YKADIGI KNGKI HGI GKAGNKDMQDGVSPHMVVGVGTEALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
Xu HH;
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Forsyth RA,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 58611; 1766pp; English.
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Carr GJ,
                                                                                                                                                                                                 2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                                                                                                                                              21-MAR-2001; 2001US-00815242
                                                                          21-MAR-2002; 2002WO-US009107
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                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zamudio C,
Trawick JD,
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Best Local Similarity
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25-OCT-2001;
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03-OCT-2002
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                                                                                                                                                                                                             481
                                                                                                                                                                                                                          533. .567
/note= "Immunogenic region. Region specifically claimed
in claim 14"
                                              VOVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
3 or
                                   LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                       TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                             IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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                                                                                                                                                                   SQAMGRAGEVI PRTWOTADKNKKEFGKI,PEDGKDNDNFRI KRYI SKYTI NPAL,THGVSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New hyperimmune serum reactive antigens from Helicobacter pylori, a encoding nucleic acid molecules, useful for diagnosing, preventing treating H. pylori infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial; antigenic; H. pylori infection.
                                                                                                                                                                                                                                                                                                               FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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                                                                                                                                                                                                                                                                                                                                                                            ADU05536 standard; protein;
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preparation (e.g. a vaccine) for treating or preventing H. pylori infections. The antigen or its fragment may also be used for isolating, purifying and/or identifying an interaction partner of the hyperimmune serum reactive antigen or fragment, for generating a peptide binding to the hyperimmune serum reactive antigen or fragment, where the peptide is selected from anticalines; for manufacturing a functional nucleic acid selected from aribozymes, antisense manufacturing a functional ribonucleic acid selected from ribozymes, antisense nucleic acids and present sequence represents the amino acid sequence of an H. pylori antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
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hyperimmune serum reactive antigen or its fragment. The composition (including the nucleic acid molecule, hyperimmune serum-reactive antigen or antibody) is useful for manufacturing a medicament or pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 VQVAIHTDTLMEAGCVEDTWAAIAGRTWHTFHTEGAGGGAAPDIIKVAGEHNILPASTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGOSNSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOVCIHTDTVNBAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPOPVYYREMFGHH
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                              Length 569;
                                                                                                                                                                                                                                                                                              75; Indels
                                                                                                                                                                                                                                                            76.6%; Score 2297; DB 8; 73.4%; Pred. No. 4.5e-38; tive 76; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS09177 standard; protein; 568

 H. pylori urease beta subunit.

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Matches 416; Conservative
                                                                                                                                                                                                                                Sequence 569 AA;
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(ORAV-) ORAVAX INC.
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                                                                                                                                                                                                                                                                                      attricture of the beta-subunit Helicobacter pylori urease, appearing as ADS09176 (amino acids 201-338 of the beta subunit) or a sequence which generates antibodies that suppresses proliferation of H. Pylori and which suppresses proliferation of H. Pylori and which suppresses urease activity of H. Pylori by an immune reaction. Also included are a gene which encodes the urease fragment, a vaccine against H. Pylori comprising the urease fragment, a transformed cell transformed by introducing the gene, an antibody which recognises the urease fragment and transforming a plant by introducing the gene into the plant and making it express. The urease fragment is useful for producing blood serum containing antibodies which suppresses proliferation of H. Pylori and which suppresses urease activity of H. Pylori which involves immunising a living organism (e.g. a human, cow or hen) with the urease immunising a living organism (e.g. a human, cow or hen) with the urease is transgenic animals expressing the fragment. H. Pylori is thought to be a cause of gastric and peptic ulcers, gastritis and may be implicated in stomach cancer. The urease enzyme is thought to be responsible for maintaining the bacterium in the acid conditions of the stomach. The present sequence is the H. Pylori urease beta subunit from which the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                  Protein having specific region of beta-subunit urease of Helicobacter pylori, which generates antibodies that suppress proliferation and urease activity of bacteria, useful for preventing Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                 The invention relates to a protein having a specific region of primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KWKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 XISRXEYVSMYGPTTGDKVRLGDTDLIAEVEHDYTIYGEELKPGGGKTLREGMSQSNNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 VQVAIHTDTLNEAGCVEDTMAAIAGRTMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRAAEEYSMINGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.1%; Score 2282; DB 8; Length 568; 73.1%; Pred. No. 9.1e-38; ive 77; Mismatches 75; Indels
                                                                                                                                                DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
FUKUYAMA RINSHO KENSA CENT KK.
                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 2; 26pp; Japanese.
                                                                                                                       28-FEB-2003; 2003JP-00054654.
                                                                                            28-FEB-2003; 2003JP-00054654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.1
Best Local Similarity 73.1
Matches 413; Conservative
              Helicobacter pylori
                                                                                                                                                                                      WPI; 2004-665475/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 568 AA;
                                     JP2004261080-A.
                                                                  24-SEP-2004
                                                                                                                                                                                                                                                             infection.
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a Helicobacter antigen, and parenterally administering to the mammal a comprising anticle action molecule another antigen. Also included is an attenuated Salmonella vector comprising a mucleic acid molecule encoding a Helicobacter antigen. The Helicobacter antigen is a urease, a urease subunit, or its immunogenic fragment (encoded by the ureA and ureB genes). The mammal is at risk of thaving but does not have Helicobacter infection or has a Helicobacter in a mammal. The vector further comprises an hirA or infection. The attenuated Salmonella vector further comprises an hirA or infection. The vector and be used to treat Helicobacter infection. The vector and the method can be used to treat Helicobacter infection. The vector and the method can be used to treat Helicobacter induced gastroducdenal diseases, including acute, chronic or atrophic gastritis, peptic ulcer diseases (e.g. gastric or ducdenal culcers), and gastric carcinoma. Attenuated Salmonella vector pHUR3 was constructed expressing UreA and UreB and including an B. coli AmpR gene. The present sequence represents a protein or peptide encoded by the pHUR3
                                                                                422
                                                                                                                                                                     481
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                                        SQAMGRAGEVI PRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                     422 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                                                                                                                                                                                          GKAKFDISITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pHUR3; vaccine; helicobacter pylori infection; urease; immune stimulation; antibacterial; Immunostimulant; antiulcer; cytostatic; antinflammatory; gastrointestinal-gen.; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hylicobacter pylori Urase B protein fragment SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kleanthous H, Londono-Arcila P, Freeman D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 5; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEVFVDGKLCTSKPTSQVPLAQRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 YHVFVDGKEVTSKPANKVSLAQLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEB55116 standard; protein; 570 AA.
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N-PSDB; AEB55112, AEB55130
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19-MAY-1993;
19-NOV-1993;
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plasmid. NOTE: pHUR3 is represented by both AEB55112 and AEB55130, the peptides expressed by pHUR3 are shown in the sequence listing to be split between AEB55112 and AEB55130, yet Figure 4 shows all the peptides being expressed by the one sequence, therefore all encoded peptides are cross-
                                                                                                                                     238
                                                                                                                                                                                                                                                          300
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                                                                                                                                                                                                                                                                                                                                               478
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                                                                                                                                                                                                                                                                                                                                                                                          481 AHHGKAKYDANITFVSQAAYDKGIKEELGLERQVLPVKNCRNITKKDMQFNDTTAHIEVN 540
                                                                                                                     9
                                                                                                              EYDVQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSS
                                                                                                                                                                                                                                                   TNPTIPFTVNTEAEHMDMLMVCHHLDKSIKEDVQFADSRIRPQTIAAEDTLHDMGIFSIT
                                                                                                                                                                                                                                                                                                                      Urease; ureB gene; immunogen; vaccine; diagnostic; Helicobacter felis.
                                                                                                                                                                        ALAGEGMI ITAGGI DSHTHFLS PQQF PTALANGVTTMFGGGTGPVDGTNATTI TPGKWNL
                                                                                                                                                                                                          HRMLRAAEEYSMIVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVAD
                                                                                                                                                                                                                                                                           TTPT1PYTINTVAEHLDML/MTCHHLDKR1REDLOFSQSR1RPGS1AAEDVLHDMGV1AMT
                                                                                                                                                                                                                                                                                                             SSDSQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGV
                                                                                                                                                                                                                                                                                                                                               SEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMF
                                                                                                     2 KMKK---QEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSN
                                                                                     Gaps
                                                                                     3,
                                                                                     76; Indels
                                                                    Length
                                                                   76.1%; Score 2282; DB 4; 73.0%; Pred. No. 9.1e-38; iive 75; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                   PKTFEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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                                  referenced to both sequences
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(first entry)
                                                                                     tches 416; Conservative
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                                                                    Query Match
Best Local Similarity
                                                   Sequence 570 AA
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22-JUN-1995
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                                                                                                                                                                                             DNA from Helicobacter pylori and Helicobacter felis - used to develop prods. for detection, treatment and prevention of Helicobacter infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 VQVAIHTDTLMEAGCVEDTWAAIAGRTWHTFHTEGAGGGAAPDIIKVAGEHNILPASTNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%; Score 2281; DB 2;
73.0%; Pred. No. 9.5e-38;
iive 76; Mismatches 77;
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                                                                                                                 Thiberge
                                                                            RECH MEDICALE
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                                                                                                                     Ferrero
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93EP-00401309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 73.0
Matches 414; Conservative
                                                                                                                   Suerbaum S,
                                                       (INSP ) INST PASTEUR.
(INRM ) INST NAT SANTE
                                                                                                                                                        WPI; 1995-006797/01
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 569 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic composition against Helicobacter infection - also gene
fragment(s) and protein(s) from Helicobacter urease gene cluster and heat
shock protein(s).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKMNLHRM ·181
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                                                                                                             Urease; UreA; UreB; vaccine; Helicobacter infection; UreI;
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(INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                      Ferrero R;
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                                                                             Helicobacter felis urease UreB.
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Matches 411; Conservative
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                                                                                                                             heat shock protein.
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AAR74337;
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                SQAMGRVGEVITRIWQTADKNKKEFGRLKEEKGDNDNFRIKRYISKYTINPGIAHGISDY
                                                                                                                 GKAKFDTSITFVSKVAYENGVKEKLGLEROVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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974.851 Million cell updates/sec
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Sequence 6, A
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: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
: /EMC_Celerra_SIDS3/ptodata/2/iaa/PGTUS_COMB.pep:*
: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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US-09-338-920B-6
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US-08-466-248-26
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PCT-US56-05800-3
US-09-431-705-5
US-08-457-822-21
US-08-467-822-21
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US-09-338-920B-10
US-09-338-920B-10
US-09-325-991A-26897
US-08-466-248-27
US-08-466-248-27
US-08-466-248-27
US-08-48-27
US-09-489-039A-9216
US-09-489-039A-9216
US-09-489-039A-9216
US-08-667-645B-5
US-08-687-645B-5
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Match Length
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Perfect score:
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Maximum DB
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160, Appl
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3459, Ap
4843, Ap
63, Appl
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                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
TITLE OF INVENTION: Stabilization of Helicobacter Urease FILE REFERENCE: 06132/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR FILING DATE: 1997-09-12
US-08-466-248-25
US-09-134-0010--5026
US-09-602-777A-14
US-09-602-777A-16
US-09-338-9208-14
US-09-138-9208-14
US-09-583-110-4036
US-09-583-110-4036
US-09-130-433-4843
US-09-134-078-63
US-09-134-078-63
US-09-134-078-65
US-09-139-764-59
US-09-206-942-65
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US-09-206-942-65
US-09-206-942-65
US-09-206-942-65
US-10-193-764-65
US-09-206-942-65
US-09-206-942-65
US-09-206-942-65
US-09-206-942-65
US-09-206-942-65
US-09-303-682-2
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                            US-09-338-920B-12; Sequence 12, Application US/09338920B; Patent No. 6709851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter heilmannii
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Best Local Similarity 73.73
Matches 418; Conservative
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GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT 541
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APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES ITILE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
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543 YHVFVDGKEVTSKPANKVSLAQLFSIF 569
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APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                Sequence 26, Application US/08467822
Patent No. 5843460
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELBEAK: (202) 408-4400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                       362 SQAMGRVGEVITRIWQTADKOKKEFGRLPEEKGDNDNFRIKRYISKYTINPAITHGISEY 421
                                                                                                                            GKAKFDĮSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT 541
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                                                                                                   IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH 481
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                        SQAMGRAGEVI PRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06131/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR PILING DATE: 1005: 14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                               542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                      542 YKVKVDGNEVTSHAADKLSLAQLYNLF 568
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Patent No. 6709851
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TYPE: PRT
ORGANISM: Helicobacter pylori
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US-09-338-920B-6
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TOPOLOGY:
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APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: DOLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                             GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT 541
 62
                                        KISRKEYVSMYGPTTGDKVRLGDTDLIAEVEHDYTIYGEBLKFGGGKTLREGMSQSNNPS
                                                                              GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM
                                                                                                                                                                                        VQVCIHTDTVNBAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
                          ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA
                                                                                                                                    LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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                                                                                                                                                                                                                                                                                                 SQAMGRAGEVI PRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALISE FORCE:
WEBLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/08432697
Patent No. 6248330
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COMPUTER READABLE FORM:
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GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Retrero, Richard L.
APPLICANT: Priberge, Jean-Michel
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCES: 44
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REFERENCE/DOCKET NUMBER: 03495.0137-00000
TELECHOMINICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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YHVFVDGKEVTSKPANKVSLAQLFSIF 569
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                                                                                                                                                                                                            STRANDEDNESS: single
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123 GEGLIVTAGGIDTHIHFISPQQIPTAPASGVTTMIGGGTGPADGTNATTITPGRRNLKWM 182
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                                                                GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08920095
Patent No. 5837240
BAPPLICANT: Cynthia K. Lee et al.
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

REDUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATR:

APPLICATION NUMBER: US/08/920,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/013001
TELECOMMUTCATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                           542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                  US/08/431,041
                                                                                                                                                                                                                                                                                                                                                                                                                           E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 73.6%
Matches 415; Conservative
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CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                 US-08-920-095-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD 61
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                                                                                                                ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: DEP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 569 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-466-248-26
                                                                                                    COUNTRY:
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VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTTP 301
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                                                                              SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                       SQAMGRVGEVITRTWQTADKAKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY
                                                                                                                                                                                                                                              GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
                                                                                                                                                                                  IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application PC/TUS9605800
GENERAL INFORMATION:
APPLICANT: OraVax, Inc.
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05800
FILING DATE: 23-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REPERENCE/DOCKET NUMBER: 06132/020001
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                           542 FEVFVDGKLCTSKPTSQVPLAQRY 565
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,041
FILLING DATE: 28-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/568,122
FILLING DATE: 06-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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amino acid
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ZIP: 02110-2804
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76.4%; Score 2290; DB 5; Length 566;

Query Match

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                                                                                                                                         62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA
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                              Gaps
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Patent No. 6585975

GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Londono-Arcila, Patricia
APPLICANT: Freeman, Donna
TITLE OF INVENTION: Use of salmonella vectors for
TITLE OF INVENTION: Vaccination against helicobacter infection
FILE REFERENCE: 06132/06001
CURRENT FILING DATE: 1999-11-01
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 52

COFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2e-40;
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       73.6%; Pred. No.
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US-09-431-705-5
         Best Local Similarity 73.6
Matches 415; Conservative
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Best Local Similarity 73.0
Matches 416; Conservative
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US-09-431-705-5
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SEQ ID NO 5
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Patent No. 5843460
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero', Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDSQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGI 420
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SPDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTE 118
                                ALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGFVDGTNATTITFGKWNL 178
                                                                                                                                                                        HEMILRAABEYSMNVGFLGKGNSSSKKQLVEQVBAGAIGFKLHBDWGTTPSAIDHCLSVAD 238
                                                                                                                                                                                                                                                                                                             EYDVQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSS 298
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKTFEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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PETYHVFVDGKEVTSKPANKVSLAQLFSIF 570
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
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243 VQVAIHTDTLNEAGCVEDTLEAIAGRTIHTFHTEGAGGGHAPDVIKMAGEFNILPASTNP 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 SQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYISKYTINPGIAHGISDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 GKNKFDTNITFVSQAAYRAGIKEELGLDRAAPPVKNCRNITKKDLKFNDVTAHIDVNPET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
LOCATION: 1..569
OTHER INFORMATION: /note= "URE B - FIGURE 3."
                                                                                  REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REPERENCE/POCKET NUMBER: 03495.0137-02000
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
LENDTH: 569 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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    US 08/432,697
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US-08-432-697-21
; Sequence 21, Application US/08432697
; Batent No. 6246330
; GENERAL INFORMATION:
                        02-MAY-1995
N: 435
                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
APPLICATION NUMBER:
FILING DATE: 02-MAN
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastien

APPLICANT: Ferrero, Richard L.

APPLICANT: Friberge, Jean-Michel

TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
                     363 SQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYISKYTINPGIAHGISDY
                                                                                                                                                                                            483 GKNKFDTNITFVSQAAYKAGIKEELGLDRAAPPVKNCRNITKKDLKFNDVTAHIDVNPET
                                                                                                                                                                    482 GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKŢ
SQAMGRAGEVIPRIWQIADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                 422 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                     542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                               Sequence 21, Application US/08466248 Patent No. 6258359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
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          APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNGERIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Punner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRANLKSM 182
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                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3315
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: O2-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.8%; Score 2244; DB 2; Best Local Similarity 72.5%; Pred. No. 1.8e-39; Matches 411; Conservative 71; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein

1 COCATION: 1..569

1 OTHER INPORMATION: /note= "URB B - FIGURE 3."

102-08-432-697-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
EFFERENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION: INPORMATION:
TELEPHONE: (202) 408-4000
Sauerbaum, Sebastien
Ferrero, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 569 amino acids TYPE: amino acid
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MOLECULE TYPE: peptide
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411; Conservative
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US-09-338-920B-8
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                                                                                                                                                                                     SYELDLVIJINALIVDYTGIXKADIGIKDGKIAGIGKAGNKDMQDGVDNNLCVGPATEALA 122
                                                                                                                                                                                                                                            62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTBALA 121
                                                                                                                                                                                                                             122 GEGMIITAGGIDSHTHFLSPQQPPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
                                                                                                                                                                                                                                                                                     LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADBYD 241
                                                                                                                                                                                                                                                                                                                                           VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTTP 301
                                                                                                                                                                                                                                                                                                                                                           243 VQVAIHTDTLNEAGCVEDTLEAIAGRTIHTFHTEGAGGGHAPDVIKWAGEFNILPASTNP 302
                                                                                                                                                                                                                                                                                                                                                                                                   TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD 361
                                                                                                                                                                                                                                                                                                                                                                                                                  TIPFIKATEAEHMDMLMVCHHLDKSIKEDVQFADSRIRPQTIAAEDQLHDMGIPSITSSD 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGSVEEGKIADLUVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH 481
                                                                                                                              KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                                                                      Gaps
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Pred. No. 1.8e-39;
                                                          Length 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
APPLICANT: Monath, Thomas D., Jr.
APPLICANT: Monath, Thomas D., Jr.
TITLE OF INVEXTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06132/02302
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING APTE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR PILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 100
                                                      74.8%; Score 2244; DB 2; Length 5 72.5%; Pred. No. 1.8e-39; ive 71; Mismatches 85; Indels
                - FIGURE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                m
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; LOCATION: 1..569
; OTHER INFORMATION: /note= "URE
US-08-466-248-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.8%;
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TYPE: PRT
COGGANISM: Helicobacter felis
US-09-338-9208-10
                                                    Query Match 74.8%;
Best Local Similarity 72.5%;
Matches 411; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-338-920B-10
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                                       2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEBLKFGAGKTIREGMGQSNSPD
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APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas William D., Jr.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILER REFERENCE: 06132/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR PLLING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S
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85;
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71; Mismatches
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US-09-338-920B-8
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Best Local Similarity 73.2
Matches 406, Conservative
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                                                             GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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                                                                                                                                          VOVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 0.72mb
CMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72mb
CMPUTER: 1BM PC compatible (NEC PC-9801 RX)
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII Form
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,242C
FILING DATE: 19910718
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/732,242C
FILING DATE: 19910718
FILING DATE: 19910718
FILING DATE: 10-MG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Herbert
REGISTRATION NUMBER: 17081
RESTERNCE/DOCKET NUMBER: 910532/HG
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5298399
GENERAL INFORMATION:
APPLICANT: UOCANTICALE MASARI, HATUHIKO;
APPLICANT: Hidaka, Makoto; Nakamura, Akira;
APPLICANT: Maeda, Michihisa; Yoneta, Yasuo;
TITLE OF INVENTION: Gene of Urease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frishauf, Holtz, Goodman & Woodward.
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543 YHVFVDGKEVTLNQP 557
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Sequence 26817, Application US/09252991A
Sequence 26817, Application US/09252991A
Sequence 26817, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICAMT:
Marc J. Rubenfield et al.
TITLE OF INVENTION:
NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
APPLICAMTON: APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26887
LENGTH: 566
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                                                                                                                                                                                                                                          Length 568;
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INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino
                                                                                 LENGTH: 568 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.4%
Matches 378; Conservative
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MOLECULE TYPE: peptide
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                                                                                    6; Gaps
                                                       Query Match 61.2%; Score 1834; DB 2; Length 566; Best Local Similarity 59.1%; Pred. No. 6.6e-31; Matches 337; Conservative 87; Mismatches 140; Indels
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26887
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Search completed: August 9, 2006, 21:44:42 Job time : 53 secs

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Sequence 15, Appli
Sequence 12, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 252, App
Sequence 252, App
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19, Appl
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                                                                                 (without alignments)
1422.195 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/USIO8_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/USIO8_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/USIO8_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39
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                                                                     9, 2006, 21:44:02; Search time 185 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-904-994B-15
US-09-904-994B-6
US-09-904-994B-6
US-09-904-994B-9
US-10-639-273-3
US-10-639-273-3
US-10-282-122A-58611
US-10-282-122A-58611
US-10-282-122A-976-8
US-10-282-122A-4763-8
US-10-282-122A-49766
US-10-282-122A-69766
US-10-282-122A-66743
US-10-282-122A-66743
US-10-282-122A-66823
US-10-282-122A-66833
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US-10-282-122A-66833
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                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA_Main:*
                                                                                                                                                                                                     2097797 seqs, 463214858 residues
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Listing first 45 summaries

    protein search, using sw model

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seq length: 200000000
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64617, A	sequence	US-10-282-122A-64617	4	577	54.2	1624	45
62532, A	Sequence	US-10-282-122A-62532	4	577	54.2	1624	4
16, Appl	Sequence	US-10-454-437-16	Ŋ	534	54.4	1631	43
14635, A	Sequence	US-10-156-761-14635	4	573	56.9	1706	42
51072, A	Sequence	US-10-282-122A-51072	4	571	57.1	1713	41
	Sequence	US-10-454-437-14	Ŋ	570	57.4	1720	40
76849, A	Sequence	US-10-282-122A-76849	4	598	57.4	1721	39
2, Appli	Sequence	US-10-418-962-2	4	837	57.6	1726	38
3599, Ap	Sequence	US-09-738-626-3599	ო	570	57.6	1728	37
124057,	Sequence	US-10-437-963-124057	4	843	59.0	1769	36
1, Appli	Sequence	US-11-046-271-1	9	840	59.0	1770	35
1, Appli	Sequence	US-10-731-877-1	'n	840	59.0	1770	34
7, Appli	Sequence	US-10-621-833-7	4	840	59.0	1770	33
78027, A	Sequence	US-10-282-122A-78027	4	572	59.9	1795	32
44443, A	Sequence	US-10-282-122A-44443	4	571	59.9	1797	31
6526, Ap	Sequence	US-10-724-972A-6526	4	573	60.1	1803	30
70574, A	Sequence	US-10-282-122A-70574	4	811	60.2	1804	29
118, App	Sequence	US-10-793-626-118	S	571	60.2	1804	28

ALIGNMENTS

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DENTLDEVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHWVVGVGTEAL 120
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Sequence 3, Application US/09904994B
; Publication No. US20040005325A1
; GENERAL INFORMATION:
; APPLICANT: AKZO No. US20040005325A1e1 N.V.
; TILE OF INVERTION: Helicobacter vaccine
; FILE REFERENCE: Degoedesquenties
; CURRENT APPLICATION NUMBER: US/09/904,994B
; CURRENT FILING DATE: 2001-07-13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Helicobacter felis
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Best Local Similarity 100.
Matches 568; Conservative
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541 TFEVFVDGKLCTSKPTSEVPLAORYTFF 568
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                                                             DENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEAL 120
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                                               HGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPK
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Pred. No. 7.9e-53;
4; Mismatches 2;
                                                                                                                                                          Sequence 15, Application US/09904994B
; Sequence 15, Application US/09904994B
; Publication No. US20040005325A1
; GENERAL INFORMATION:
; APPLICANT: ARZO No. US20040005325A1e1 N.V.
; TITLE OF INVENTION: Helicobacter vaccine
; FILE REPERENCE: Degoedsequenties
; CURRENT APPLICATION NUMBER: US/09/904,994B
; CURRENT PILING DATE: 201-07-13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
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98.9%;
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Matches 562; Conservative
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US-09-904-994B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 MLRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEY
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US-09-904-994B-6; Sequence 6, Application US/09904994B; Sequence 6, Application US/09904994B; Publication No. US20040005325A1; GENERAL INFORMATION: Helicobacter vaccine; TITLE OF INVENTION: Helicobacter vaccine; CURRENT APPLICATION NUMBER: US/09/904,994B; CURRENT FILING DATE: 2001-07-13; SEQ ID NOS: 21; SEQ ID NOS: 21; SEQ ID NOS: 21
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APPLICANT: ARZO No. US20040005325A1e1 N.V.; TITLE OF INVENTION: Helicobacter vaccine
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Query Match
Best Local Similarity 99.2%;
Matches 491; Conservative
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                                                                                                                                                                          Score 2953; DB 3; Length 568; Pred. No. 2e-52; 5; Mismatches 5; Indels
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Publication No. US20040005325A1
GENERAL INFORMATION:
APPLICANT: AKZO No. US20040005325A1e1 N.V.
TILE OF INVENTION: Helicobacter vaccine
FILE REFERENCE: Degoedesequenties
CURRENT APPLICATION WOMBER: US/09/904,994B
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
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FILE REFERENCE: Degoedesequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
CURRENT FILING DATE: 2011-07-13
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                          uvery Match
Best Local Similarity 98.2%;
Matches 558; Conservative
                                                                                                              TYPE: PRT
ORGANISM: Helicobacter felis
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CRGANISM: Helicobacter felis

US-09-904-994B-9
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Sequence 5, Application US/10639273
; Publication No. US20040142343A1
; Publication No. US20040142343A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; APPLICANT: Simpson, Kenneth W
; APPLICANT: Zhu, Jiaqian
; TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
; TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
; FILE REFERENCE: 19603/3881
; CURRENT PAPLICATION NUMBER: US/10/639,273
; CURRENT PILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PATENTIN VET: 2.1
; SEQ ID NO 5:
LENGTH: 569
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           Length 496;
                                                          Indels
Score 2591; DB 3;
Pred. No. 4.2e-45;
1; Mismatches 2;
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US-10-639-273-5
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Best Local Similarity 74.1<sup>3</sup>
Matches 420; Conservative
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APPLICANT: ALCARATIONS, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean Francois
APPLICANT: Tomb, Jean Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/043002
CURRENT APPLICATION NUMBER: US/09/895, 913A
CURRENT PILING DATE: 2001-06-29
PRIOR FILING DATE: 1997-06-24
361
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SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 252, Application US/09895913A
; Petent No. US20020160456A1
; GENERAL INFORMATION:
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Matches 416; Conservative
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LENGTH: 569
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Sequence 38, Application US/10639273

Publication No. US20040142343A1

SERBERAL INPORMATION:

APPLICANT: Simpson, Kenneth W

APPLICANT: Simpson, Kenneth W

TITLE OF INVENTION: HELICOBACTER BIZZOZERONII URBASE GENES AND THEIR USES:

TITLE OF INVENTION: HELICOBACTER BIZZOZERONII URBASE GENES

CURRENT FILING DATE: 2003-08-12

PRIOR APPLICATION NUMBER: 60/404,337

PRIOR FILING DATE: 2002-08-16

NUMBER OF SEQ ID NOS: 41

SOFTWARE PALENTIN VET: 2.1
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                                                                                                                  123 AEGLIVTAGGIDTHIHPISPQQIPTAFASGITTMIGGGTGPADGTNATTITPGRWNLKTM 182
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    62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
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                             GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM
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Best Local Similarity
Matches 418; Conservat
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US-10-639-273-38
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SOFTWARE: PatentIn version 3.1
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                 SEQ ID NO 58611
                                           LENGTH: 569
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TITLE OF INVEXTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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                                         243 VQVAIHTDTLMEAGCVEDTWAAIAGRTWHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP
                 LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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543 YHVFVDGKEVTSKPANKVSLAQLFSIF 569
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                     75; Indels
                                                                                                       Length
                                                                                                  76.6%; Score 2297; DB 4; 73.4%; Pred. No. 5.7e-39; ative 76; Mismatches 75;
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBW PC COmpatible
OPERATING SYSTEM: Windows NT 4.0
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
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; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-282-122A-58611
                                                                                                  Query Match
Best Local Similarity 73.4<sup>§</sup>
Matches 416; Conservative
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ORGANISM: Helicobacter pylori
                  US-10-639-273-40
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                                                                                                                                                                                                                                                     SEQ ID NO 40
LENGIH: 569
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76.6%; Score 2297; DB 4;
Best Local Similarity 73.4%; Pred. No. 5.7e-39;
Matches 416; Conservative 76; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...569
SEQUENCE DESCRIPTION: SEQ ID NO: 8611:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                   NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPRA: (617)742-4214
INFORMATION FOR SEQ ID NO: 8611:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                        APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                         LENGTH: 569 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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                                                              APPLICANT: Chang, Yung-Fu
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Shupson, Kenneth W
APPLICANT: Thu 2hu, Jiaqian
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: HO DIAGNOSTIC AND TREATMENT METHODS
FILE REPERBRICE: 19603-08-12
FRIOR PELLOR APPLICATION NUMBER: 60/404,337
FRIOR APPLICATION NUMBER: 60/404,337
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
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US-10-639-273-39
Sequence 39, Application US/10639273
; Publication No. US20040142343A1
Sequence 40, Application US/10639273; Publication No. US20040142343A1; GENERAL INFORMATION:
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LENGTH:
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APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Mediculant Simpson, Senior Simpson, Senior Simpson, Senior                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
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72.5%; Pred. No. 7e-38;
tive 71; Mismatches 85; Indels
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Patent No. US20010010934A1
GENERAL INFORMATION:
APPLICANT: Daewoong Pharmaceutical Co, LTD
APPLICANT: Kim, Byung-O
APPLICANT: Shin, Sung-Seup
APPLICANT: Shin, Sung-Seup
APPLICANT: Yu, Young-Hyo
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Helicobacter felis
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Matches 411; Conservative
GENERAL INFORMATION:
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US-09-402-100-2
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APPLICANT: CALCANT: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: UreB/CTXA2B Chimeric protein
US-09-402-100-2
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Publication No. US20040142343A1
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 FEVFVDGKLCT-SKPTSQ 558
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543 YHVFVDGKEVTLNQPIKE 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
Park, Myung-Hwan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 72.89
Matches 406; Conservative
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US-10-639-273-41
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US-10-282-122A-47638
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LENGTH: 568
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhu, Jiaqian
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
FILE REPERENCE: 19603/381
CURRENT APPLICATION NUMBER: US/10/639,273
CURRENT FILING DATE: 2003-08-12
PRIOR FILING DATE: 2003-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 41
LENGTH: 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLRAAEEYSMNVGFLGKGNSSSKKQ1, VEQVRAGAIGFKLHEDWGTTPSAIDHCLSVADEY
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                    70.3%; Score 2109; DB 4; Length 569; 68.1%; Pred. No. 4.1e-35; tive 83; Mismatches 95; Indels
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: APPLICANT: Objeen, Kari
APPLICANT: Objeen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                       TYPE: PRT
ORGANISM: Helicobacter hepaticus
                                                                                                                                                                                                                                                                  Best Local Similarity 68.19
Matches 388; Conservative
                                                                                                                                                                                                                        US-10-639-273-41
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APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Yanganoto, Robert
APPLICANT: Yau, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/03-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PRILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-02-06
PRIO
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61.3%; Pred. No. 2.2e-31;
ive 97; Mismatches 121; Indels
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 61.33
Matches 348; Conservative
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481 HGKAKEDISITEVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPK 540	481 RGGALARTSLTFVSQWAADAGIAERYGLAKRIVFVRNCRNVTKADMIHNAWRPSISVDPE 540	541 TFEVFVDGKLCTSKPTSQVPLAQRYTPF 568
481 E	481 F	541 I
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⁴⁸¹ RGGALARTSLTFVSOMAADAGIAERYGLAKRIVPVRNCRNVTKADMIHNAWRPSISVDPE 540

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Search completed: August 9, 2006, 21:47:53 Job time : 187 secs

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Sequence 33826, A
Sequence 31825, A
Sequence 37, Appl
Sequence 17, Appl
Sequence 11, Appl
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9773, Ap
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1606, Ap
3352, Ap
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-292-431-37
US-11-013-711-11
US-10-505-928-98
US-11-301-554-1815
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ALIGNMENTS

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Sequence 3300, Application US/10471571A

Publication No. US20060115490A1

GENERAL INFORMATION:
APPLICANT: CHIRON SpA

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
CURRENT PILING DATE: 2003-09-12

PRIOR PILING DATE: 2001-03-7

NUMBER OF SEQ ID NOS: 5642

SOFTWARE: SeqWin99, version 1.03

LENGTH: 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1). 7(571)
OTHER INFORMATION: urease alpha subunit
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NAME/KEY: MISC FEATURE
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DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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SOS DFVGSVEVGKGADLVLWKPSFFGAKPELVVKGGAIAWANMGDPNASIPTPEPVVMRPMFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 TDQLPINMGFTGKGNTSKPEGLAEIIKAGAMGLKLHEDWGTTPSAIDNCLSVAEDFDIQV
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                                               480 HHGKAKPDISITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDP
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                                                                                                                                                                                                                                                                            APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579FUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENTIN version 3.3
                                                                                                                540 KTFEVFVDGKLCTSKPTSQVPLAQRYTFF
                                                                                                                                   Sequence 33826, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Zea mays subsp. mays US-10-953-349-33826
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APPLICANT: ALEXANDROV, Nickclai et al.
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE: DETERMINED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTI VETSION 3.3
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414
                                                                                   360 MISSDSQAMGRVGEVITRTWQVAHRMKEQRG--PLDGDFEHNDNNRIKRYIAKYTINPAI 417
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                                                                                                                                 THGVSEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYY 474
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LDVDPQTYEVYVDGEKITSNAATELPLTQRYFLF 571
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Publication No. US20060107345A1
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US-10-953-349-33827
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LENGTH: 653
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Bio-oriented Technology Research Advancement Institution.
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               APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-LENGTH PLANT CDNA AND USES THEREOF
FULE RFFERENCE: MOA-A0205Y1-LENGTH PLANT CDNA AND USES THEREOF
FURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 843;
                                                                                                                                                                                                                                                                                                                                                                                                                   59.0%; Score 1769; DB 6; 58.1%; Pred. No. 1.3e-34; iive 91; Mismatches 137;
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APPLICANT: CHEN, Xia
APPLICANT: SESHAN, Kalpathi
APPLICANT: HUNG, Chiung-Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 58.19
Matches 333; Conservative
                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
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US-10-449-902-47195
                                                                                                                                                                                                                                                                                  SEQ ID NO 47195
LENGTH: 843
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                                                                                                                                                            APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15/9PUS2
CURRENT APPLICATION VMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
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Ublication No. US20060123505A1
GENBRAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
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Pred. No. 3.3e-35;
ETYTVTADGEVLTCQPAPTLPLSRNYFLF 784
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; Publication No. US20060107345A1
                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Zea mays subsp. mays US-10-953-349-33825
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Best Local Similarity 58.9%
Matches 335; Conservative
                                                                                                                                                   GENERAL INFORMATION:
                                                                                   JS-10-953-349-33825
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LENGTH: 841
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APPLICANT: Sasaki, Ken
APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michell H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
                                                                                                                                                                                                                                                                                                                                                                                                                    3 MKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQS---NS 59
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APPLICANT: XUE, Jianmin
APPLICANT: YU, Jieh-Juen
TITLE OF INVENTION: Attenuated Vaccine Useful for
TITLE OF INVENTION: Attenuated Vaccine Useful for
TITLE OF INVENTION: Immunizations Against Coccidioid
FILE REFERENCE: 529522000600
CURRENT APPLICATION NUMBER: US/11/292,431
CURRENT APPLICATION NUMBER: US 60/633,399
PRIOR PILING DATE: 2004-12-03
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 836
TYPE: PRI
ORGANISM: Coccidioides posadasii
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                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 57.2% Matches 327; Conservative
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FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,711
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Moraxella catarrhalis US-11-013-711-11
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Best Local Similarity 25.7%
Matches 196; Conservative
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RESULT 8 US-10-505-928-98 ; Sequence 98, Application US/10505928

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                                                                            APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REPERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR PARIOR ELING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PARENTIN 3.2
LENGTH: 572
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US-10-505-928-98
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Sequence 1815, Application US/11301554 Publication No. US20060088527A1 GENERAL INFORMATION:

US-11-301-554-1815

APPLICANT: Henderson, Robert A. APPLICANT: Wang, Tongtong

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55 GQSNSPDENTLD-LVITNAMII-DYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMV 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PYTI-NTVAEHLDMLMTCHHLDKRIREDLQFSQS-RIRPGSIAAEDVLHDMGVIAMT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 V-GVGTEALAGEGMIITAGGIDSHTHFLSPQQFPTALAN----GV-TTMFGGGTGPVD-- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GINATIIIPGKWNLHRMLRAAE----EYSMNVGFLG--KGNSSSKKQLVEQVEAG 213
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                                                                                                                                                                                                                                                                                                                            AND METHODS FOR THE THERAPY
                                                                    APPLICANT: Durham, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
APPLICANT: MCNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
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CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR FILING DATE: 2005-10-28
PRIOR FILING DATE: 2002-03-28
PRIOR PILING DATE: 2002-03-28
PRIOR FILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR APPLICATION NUMBER: US 09/702,741
PRIOR PILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-06
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SOFTWARE: FastSEQ for Windows Version 4.0
Johnson, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 210121.478C21
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295 NDQILATVNSGKKSIDGGSGVDRLELRYVNGAFTAKAENLVNTLSD-GTT---1QH---- 346
                                                                                                                            415 FTFPRAPKTITELEKKVEEIPFKKER---KF--NPDLAPG-TEKV--TREGOKGEKTIT 466
                                                                                                                                                                                                                                                                                                                           515 KLPTGEKEEVPGKPGIKONPETGDVVRPPVDSVTKYGPVKGDSIVEKEEIPP-EKERKFNP 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 SNSPDENTLDLV---ITN--AMIID--YTGIYKADIGIKNGK----IHGIGKAGNKDMQD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 AADPTE-TVTLFGAKLHNIEQYYIDGSNTG---AD-NMTGGRWNDFFQGNGGADRLDGQG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GVSPHMVVGVGTEAL-AGEGMIITAGGIDSHTHF-----LSPQQFPTAL--ANGVTTM 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 YGEDGNDKLVAGAGN-DYLSGGAGSDTLDGG-----AGDDYIITGDGNDKVLAGSG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 ADEYDVQVCIH-----TDTV----NEAGY-VDDTLNAMNGR-AIHAYHIEGAG---- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 VEAYDV----HGSNASNQFT-TLGGDDNLYGYGGDDTLRAGAGNDSIFA----GDGRDKL 397
                                                                                                                                                                                                                             337 RIRPGSIAA---EDVLHDMGV-----IAMTSSDSQAMG-RAGEVIPRTWQTADKNKKE
                                                                                                                                                                                                                                                                                               489 SITFVSK--VAYENGVKE-KLG-LER----QVL---PVKNCRNITKKDFKFNDKTAKITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 NTY-GPTKGDKVR--LGDTDLWAE-VEHDYTTYGEELKFGAGK-TIR----E---GMG-Q
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                                             359 KMR-AEYAGKTWETSITDLGLSKNQAYNFLITS--SQRWGLNQG-INANGWMRTDLKGSE
                                                                                                FGKLPE-----DGK-DNDNFRIKRYISKYTINPALTHGVSEYIGSVEEGKIADLVVW
                                                                                                                                                                                                 437 NPAFFGVK-PKIVIKGGMVVFSEMGDSNASVPTPQPV-----YYREMF--GHHGKAKFDT
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPRENER. MOA-AQ205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
FRIOR PPLICATION NUMBER: JP 2002-29369
PRIOR PPLICATION NUMBER: JP 2002-383870
PRIOR PLIING DATE: 2002-05-310
PRIOR PLIING DATE: 2002-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.3%; Score 308; DB 6; Length 1006; Best Local Similarity 25.5%; Pred. No. 57; Matches 167; Conservative 89; Mismatches 187; Indels 211;
                                                                                                                                                                                                                                                                                                                                                                                                                         D--PKTFEVFVDG----KLCTSKPTSQVPL 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41462, Application US/10449902
Publication No. US20060123505A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Oryza sativa
US-10-449-902-41462
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LENGTH: 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 WGTTPSAIDHCLSVADEYDVQVCIHTDTVNEAGYVDDT-LNAMNG-RAIHAYHIEGAGGG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 HSPDVITWAGELNILPSSTTPTIPYTINTVAEHLDMLMTCHHLDKRIRED--LQF--SQS 336
                           323 CGDLQVTG-SGH-CP--YSTAQKAVGKDNFTLIPEGVNGIEERMTVVWDKAVATGKMDEN 378
                                                                                                                            379 ----QFVAVTSTNAAKIFNLYPRKGRIAVGSDADVVIWDPDKLKTITAKSHKSAVEYNIF 434
                                                                                                                                                                                                                          --KAKFDTSITFV-SKVAYEN---GVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKIT 536
                                                                                                                                                                                                                                                                                                                           KSEVTSNKOTIEHEPSVKAEDISKKEDTPKEVADV-AEVQPKSSVTHNAE----TPK-VR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 VSPHMVVGVGTEALAGEGMIITAGGID--SHTHFLSPQQFPTALANGVTTMFGGGTGPVD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTNATTITPGKWNLHRMLRA-AEEYSMNVGFLG-KGNSSSKKQLVEQVEAGAIGFKLHED 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQEYV-N--T--YGPT-KGDKV-RLGDT-----DLWAEVE-HDYTTYGEELKFGAGKTIR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRIKRYISKYTINPALTHGVSEYIGSVEEGKIADLVVWNP-------A----F
                                                                                                                                                                                              441 FGVK----PKIVIKGGMVVFSEMGDSNAS-----VPT---PQPVYYR-----EMFGHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHIRON: SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE: PO26927W0
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR APPLICATION NUMBER: GB-0107661.1
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.3%; Score 309; DB 6; Length 1629; Best Local Similarity 25.6%; Pred. No. 1.7e+02; Matches 161; Conservative 80; Mismatches 199; Indels 190;
359 SSDSQAMGRAGEVIPRTWQTADK -- NKKEFGKLPE-
                                                                                                                                                                                                                                                                                                                                                                                               537 VD--P-KTFEVFV---DGKLCTSKPTS 557
                                                                                                                                                                                                                                                                                                                                                                                                                                          548 -DNNPRRİGHRIVAPPGGR----SNITS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)._(1629)
; OTHER INFORMATION: hypothetical protein US-10-471-571A-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3542, Application US/10471571A Publication No. US20060115490A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE LOCATION: (1)...(1629)
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US-10-471-571A-3542
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APPLICANT: LOUCKA, JIRINA
APPLICANT: OSICKA, RADIM
TITLE OF INVENTION: LACKING CD11B/CD18 INTERACTION DOMAIN AND USES THEREOF
FILE REFERENCE: 2356.0096
CURRENT APPLICATION NUMBER: US/11/304,590
CURRENT FILING DATE: 2005-12-16
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-G--GHSPDVITMAGELNILPSSTTPTIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQ 335
                                                                   SR----IRPGSIAAE-DVLHDMGVIAMTSSDSQAMGRAGEVIPRTW-QTADKNKKEFGKL 389
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                   398 YGEAGN--DIMFAQGEKDVLDGGT-----GIDT-A-YL-----YVD-NYSQSMSFSV
                                                                                        ---GKGGDLLDAGIGRDYVNGGAGDDRIMDMGGDNTLIGG--DGNDEV-DITVMEKSSDG
                                                                                                                                                                                                           VKPKIVIKGG--MVVFSE-MGDSNASVPTP--QPVYYREMFGHHGKAKFDTSITFV-SKV
                                                                                                                                      390 PEDGKDND--NFRIKR-YISKYTINPALTH--GVSEYIGSVEEG--KIADLVVWNPAFFG
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LADANT, DANIEL
BAUCHE, CECILE
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PRIOR APPLICATION NUMBER: PCT/EP04/07811
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PRIOR APPLICATION NUMBER: EP 03291486.3
PRIOR FILING DATE: 2003-06-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 3.3
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Publication No. US20060159697A1
GENERAL INFORMATION:
APPLICANT: LBCLERC, CLAUDE
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Best Local Similarity 24.99
Matches 168; Conservative
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24.9%; Pred. No. 8.6e+03;
ive 93; Mismatches 207; Indels 248;
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TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53629)B

CURRENT PPLICATION NUMBER: US/11/330,403

CURRENT FILING DATE: 2006-01-12

NUMBER OF SEQ ID NOS: 19250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9773, Application US/11330403 Publication No. US20060159563A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Magnetococcus sp. MC-1
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1685 AAPPAARVPDTLMQ 1698
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Best Local Similarity 24.9%
Matches 182; Conservative
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	Qy 208 EQVEAGAIGFKLHEDW-GTTPSAIDHCLSVA-DEYDVQVCIHTDTVNEAGYVDDTLNAMN 265	Qy 266 GRAI-HAYHIBGAGGGHSPDVITWAGELNILPSSTTPTIPYTINTVAEHLDMLMTCHHLD 324 : :	OY 325 KRIREDLOFSGSRIRPGSIAAEDVLHDMGVIAMISS 360 	Qy 361 DSQAMGRAGEVIPRTWQTADKKNKKEFGKLPEDGKDNDNF 399 	Qy 400 RIKRYISKYTINPALTHGUSEXIGS-VEEGKIADLV-VWNPAFFGVKPKIV 448	Qy 449 IKGGMVVFSEMGDSNASVPTPQPVYYREMFGHHGKAKFDTSITFVSKVA 497	Qy 498 YENGVKEKLGLERQVLPVKNCRNITKKDF-KFNDKTAKITVDPKTFEVFVDGKLCTSK 554	Oy 555 PTSQVPLAOR 564 Db 789 -NAQARR 794	GENES et al.	Query Match 10.1%; Score 303; DB 6; Length 4834; Best Local Similarity 22.9%; Pred. No. 3.5e+03; Matches 157; Conservative 117; Mismatches 212; Indels 201; Gaps 85;	Qy 8 YVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFG 45	Qy 46 AGKTIREG-MGQSN-SP-DE-NTLDLVITNAMIIDYTGIYKADIG-IKN-GKIHG 94 : : :: :	Qy 95 -IGKAGNKDMQDGVSPHMVVGVGTEALAGEGMI-ITAGGIDSHTHFLSPQQFPTALANGV 152	Qy 153 TTMFG-GGT-GPVDGTNATTITPG-KWNLHRMLRAAEEYSMNVG-FLGKG 198
Db 5282 DIIKIWSTTTSEDMIFGDNAYILRAQNEASSSDQNWMLQAKTLVNDKG-GDDTIITGSGG 5340	Qy 267 RAIHAYHIEGAGGGISPDVITWAGELN-ILPSSTTPTIPYTINTV 310 ::	QY 311 AEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDW-GVIAMTS-SDSQAMGRA 368 ::	QY 369 GEVIPRTWQTADKNKKEFGKL-PEDGKDNDNFRIKRYISKYTINP 412	QY 413 ALTHGV-SEYIGSVEEGKIA-DLVVWNPAFFGVKPKIVIKGGWVVFSEMG 460	Qy 461 DSNASVPTDQPVYYREMFGHHGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVK 516	Qy 517NCRNİTKOFKFNDKTAKITVDFKTFEV-FVDGKLCTSKPİSQV 559	Qy 560PLAQRYTF 567 Db 5653 GDPPNQRFAF 5662	RESULT 14 US-10-471-571A-5160 Semence 5160 Annication HS/10471571A	Publication No GENERAL INFORM APPLICANT: CH TITLE OF INVE FILE REFERENC CURRENT FILIN PRIOR APPLICA PRIOR PILING NUMBER OF SEG SOFTWARE: SEG SOFTWARE: SEG SOFTWARE: SEG SOFTWARE: SEG SOFTWARE: SEG SOFTWARE: SEG SOFTWARE: SEG SOFTWARE: SEG SOFTWARE: SEG LENGTH: 801 TYPE: PRT ORGANISM: ST FRATURE: NET ORGANISM: NET ORGANISM: NET ORGANISM: NET ORGANISM: NET	Query Match 10.1%; Score 303; DB 6; Length 801; Best Local Similarity 25.5%; Pred. No. 43; Matches 171; Conservative 83; Mismatches 172; Indels 244; Gaps 84;	Qy 9 VNTYGPTKGDKVRLGDTDLMAE-VEHDYTTYGEELKFGAGKTIREGMGQS 57	Qy 58 NSPDENTLDLVITNAMIID-YTGIYKADIGIKNGKIHGIGKAG 99 133 GSTTFTSLKVSGCDLYSAGQIVENABIKGIEIFNSVDNNYK-KIFLKDGNVVGAVLYG 369	Qy 100 NKDMQDGVSPHMV-VGVGTEALAGEGMIITAGGIDSHTHFLSPQQFPTA-LANGVT 153	QY 154 TMFGGGTGPVD-GTNATTITP-GKWNLHRMLRAABEYSMNVGFLGK-GNSSSK-KQLV 207

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4174 YGKLGRGGSDGCKVPMKIDSLIGLGVVKVECGSQFSV-ALTKSGAVYTWGKGDYHRLGHG 4232
                                                                                                                                                                                                                                                 : | | ||: | : | : | : | : | 332
4281 LGDGTTNAIQRPRLVAA--LQGKKVNRVACGSAH-----TLAWGTS-KPASAGKLPAQVP 4332
                                                                                                                                                                                                                                                                                                                             | :: :| : | | | | | :: | | | | 444 FGQMCAKMSSF--GPDSLLLPHRVWKVKFVGESVDDCGGGGSESIABICEELQN----GL 4497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4544 IRTGSPLSLNLAEPVWKQLAGMSLTIADLSEV-DKDFIPGLMYIRDNEATS-----EEF 4596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 V-DDTLNAM-NGRAIHAYHIEG-----AGGGHSPDVITWAGELNILPSST--TPT-IP 304
                                                                                                                                                                                                                        305 YTINTVAE----HL-DMLMTCHHLDKR----I-REDLOFS--OSRIRPGSIAAEDVLHDM 352
                                                                                                                                                                                                                                                                                                      353 GVIAMTSSDS-----QA-MGR---AGEVIP--RIWQTADKNKKEFGKL--PEDGKDNDN 398
                                                                                                                                                                                                                                                                                                                                                                                399 F-RIKRYISKYTINP---ALTHGV--SEYIG-SVEE---G---KIADLV--VWNPAFFGV 443
                                                             199 NSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYDVQVCIHT--DTVNEAGY 256
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Search completed: August 9, 2006, 21:48:34 Job time : 36 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

August 9, 2006, 21:38:07; Search time 41 Seconds (without alignments) 1332.954 Million cell updates/sec

US-09-904-994B-3 2999 1 MKWKKQEYVNTYGPTKGDKV......KLCTSKPTSQVPLAQRYTFF 568 Title:

Perfect score:

Sequence:

Gapop 4.0 , Gapext 1.0

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pir 80:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ase (EC 3	urease (EC 3.5.1.5		urease alpha subun	urease (alpha subu	urease (EC 3.5.1.5	ŭ	urease (EC 3.5.1.5	urease, alpha subu	urease (EC 3.5.1.5	urease alpha subun	urease (EC 3.5.1.5	ij	urease (EC 3.5.1.5	urease (EC 3.5.1.5	probable urease st	urease alpha subun		urease alpha subun	probable urease F1	urease (EC 3.5.1.5	urease alpha subun	urease (EC 3.5.1.5	3.5.1.	urease (EC 3.5.1.5	3.5.1.	urease (EC 3.5.1.5	urease complex com	urease (EC 3.5.1.5
SUMMARIES																														
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do	Query Match	76.6	74.8	68.2	٠	9.99	64.8	63.9	63.4	61.7	61.5	61.3	61.3	61.2	60.09	60.8	9.09		60.5	60.5	٠		59.9	6	ď.	59.0	57.8	57.8		57.3
	Score	2297	2244	2044	2027	1998	1942	1916	1900	1849	1843	1838	1838	1834	1826	1822	1818	1818	1814	1814	1805	1801	1797	1795	1792	1770	1734	73	1721	1717
	Result No.	-	7	3	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		29

probable ureC prot	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease (EC 3.5.1.5	puative autotransp	hyaluronate lyase	dihydroorotase [im	hyaluronidase [imp	hypothetical prote	adenine deaminases	aconitate hydratas	aconitate hydratas	d-aminoacylase (as	ABC-type transport	hypothetical prote
B70665	S10032	T29056	T50711	T08993	AD0548	F97907	H96963	B95037	G86643	AD1664	AD2906	E97681	B75202	C48399	T20371
8	Н	N	~	7	N	~	7	7	~	~	~	~	7	~	7
577	614	558	569	129	196	1078	424	1066	1983	579	897	897	526	2020	2198
54.2	51.7	42.2	40.7	14.7	11.3	11.1	11.1	11.0	11.0	10.9	10.9	10.9	10.8	10.8	10.8
1624	1549	1266	1222	441	339	333	332	331	329	328	326	326	325	324	324
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	urease (BC 3.5.1.5) 62K chain - Helicobacter pylori (strains 26695, J99, and others) NyAlternate names: urease beta chain; urease chain B; urease large subunit Conscise: Haliobarter wylori
	C./Date: 30-Sep-1991 #sequence revision 02-Dec-1994 #text change 05-Oct-2004 C./Accession: B38537; H64528; Ā71977; F41834; S07885; S12487; A49215; B61371; A35306; B41E
	RiLabigne, A.; Cussac, V.; Courcoux, P. J. Bacteriol. 173, 1920-1931, 1991 A. mitti. Chuttle, classic and misloceid commons of Bolischearer wilder person resonativi
	Ajitie: Judite Lighting and incloude Sequences of mellocacie, pilot genes responsibly AjReferoce number: A38537; MUID:91161505; PMID:2001995 AjAccession: B38537
	A,Molecule type: DNA A.Residnes: 1-569 (LAB)
	A,Cross-references: UNIPROT:P14917; UNIPARC:UPI000002C20A; GB:M60398; NID:g149007; PIDN:P. P. White C. Weiler D. P. Clarton D. S. Cutton C. C. Flaischmann P. D.
	Peterson, 5.: Influs, B.: Richardson, D.: Dodson, R.: Khalak, H.G.: Glodek, A.: McKenney
	son, σ.υ.; κειιεγ, σ.m.; cocton, m.υ.; weldman, σ.m.; rujll, c.; sowman, c.; wattney, ω. Nature 388, 539-547, 1997
,	A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A a.Title. The complete canone semience of the castric nathogen Helicharter polori
	A)Reference number: A64520; MUID:97394467; PMID:9252185
	A; Accession: H64528 b. Cratus. muclair arid semience not shown translation not shown
	A; Molecule type: DNA
	A;Residues: 1-569 <tom></tom>
	A;Gross=referances: UNIPARC(UF1000002C20A; GB:AB000529; GB:AB000511; NID:g2313152; PIDN:/ A.graevimental mouvre. atrain 26696
	; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; ¹ Nature 397. 176-180. 1999
	A, Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
	A. Reference number: A71800; MUID: 99120557; PMID: 9923682
	#Ancesision: Allor. A: Molecule type: DNA
	A/Residues: 1-569 <arn></arn>
	A/;Cross-Terebrances: UNIPARC.UPLUUUUUZCZUA; GB:ABUUL446; GB:ABUUL439; NID:G915345/3; FIDN:/ A/:Experimental source: Strain J99
	R; Cussac, V.; Ferrero, R.L.; Labigne, A.
	. baccettol. 1/4, 44be-44/3, 1992 a.mitle. Rymression of Halicobacter ovlori urease genes in Rscherichia coli grown under r
	A41834; MUID:92210488; PMID:1313413
	A.Accession: F41834
	A;Ocacus: preliminary A;Molecule type: DNA
	A.Residues: 565-569 (CUS>
	A;cross-rererences: UNIFAKC:UF1UUUUZDZAD; GB:M84338 R;Clayton, C.L.; Pallen, M.J.; Kleanthous, H.; Wren, B.W.; Tabaqchali, S.
	A;Iltie: Nucleotide Bequence or two genes from Hellcobacter pylori encoding for urease st A;Reference number: S07884; MUID:90221820; PMID:2326167
_	A;Accession: S07885

421 422 481 482 541

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A)Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and two C; Superfamily: urease, alpha subunit; urease 62K chain homology C; Superfamily: urease, alpha subunit; urease 62K chain homology C; Superfamily: urease 62K chain #status experimental <MAT>
F; 1-569/Product: urease 62K chain homology <U62>
F; 136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted F; 219,248,274/Binding site: nickel 1 (Lys) His, His) #status predicted F; 219,248,274/Binding site: carbon dioxide (Lys) (covalent) (by urease activase) #status predicter F; 221,322/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:Q08716; UNIPARC:UPI000002F34B; EMBL:X69080; NID:g396160; PIDM
                                                                183 LRAABEYSMNIGFLAKGNASNDASLADQIEAGAIGFKIHEDWGTTPSAINHALDVADKYD 242
                                                                                                                                                                             243 VQVAIHTDTLNEAGCVEDTWAAIAGRTWHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Cloning, expression and sequencing of Helicobacter felis urease genes. A,Reference number: S35290; MUID:94018627; PMID:8412683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKOMQDGVSPHMVVGVGTEALA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      urease (BC 3.5.1.5) 62K chain - Helicobacter felis
NiAlternate names: urease beta chain
CiSpecies: Helicobacter felis
CiBote: 31.Dec-1993 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                 TIPFTVNTEAEHMDMLMVCHHLDKSIKEDVQFADSRIRPQTIAAEDTLHDMGIFSITSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                            VOVCIHTDIVNEAGYVDDILNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
                                                                                                                                                                                                                                                   TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                                                                                                                                                                          SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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Pred. No. 3.5e-45;
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y 72.5%; Pred. No. 3....
71; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: 835291
R;Ferrero, R.L.; Labigne, A.
Mol. Microbiol. 9, 323-333, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 411; Conservative
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Best Local Similarity
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A; Residues: 1-9,'A',11-103,'T',105-180,'F',182-192,'F',194-217,'L',219-272,'Y',274-539,'
A; Cross-references: UNIPARC:UPI00002DB18; EMBL:X17079; NID:g43633; PIDN:CAA34933.1; PID
R; Turbett, G.R.; Hoj. P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A; Title: Purification and characterization of the urease enzymes of Helicobacter species
A; Reference number: A49215; MUID:93084378; PMID:1452359
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A; Molecule type: DNA
A;Residues: 1-9,'A',11-18,'A',20-103,'T',105-180,'F',182-192,'F',194-217,'L',219-272,'Y'
A;Cross-references: UNIPARC:UPI0000172DA6; EMBL:X17079
R;Clayron, C.L.
submitted to the EMBL Data Library, October 1989
A;Reference number: S12487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Experimental source: strain NCTC 11637
A, Note: sequence extracted from NCBI backbone (NCBIP:119482)'
R, Svans Jr., D.J.; Evans, D.G.; Kirkpatrick, S.S.; Graham, D.Y.
Microb. Pathog. 10, 15-26, 1991
A, Title: Characterization of the Helicobacter pylori urease and purification of its subu A, Reference number: A61371; MUID:91312104; PMID:1857197
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R;Hu, L.T.; Mobley, H.L.T.
Infect: Immun. 58, 932-998, 1990
A;Title: Immun. 58, 922-998, 1990
A;Title: Purification and N-terminal analysis of urease from Helicobacter pylori.
A;Reference number: A41502; MUID:90202165; PMID:2318539
A;Accession: B41502
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A; Readudes: 1-21, C', 23-26, C', 28, 'I', 30 <EVA>
A; Readudes: 1-21, C', 23-26, 'C', 28, 'I', 30 <EVA>
A; Cross-references: UNIPARC: UPI0000172DA7
B; Dunn, B.E.; Campbell, G.P.; Perez-Perez, G.I.; Blaser, M.J.
J. Biol. Chem. 265, 9464-9468, 1990
A; Title: Purification and characterization of urease from Helicobacter pylori.
A; Reference number: A35306, MUID: 90264448; PMID: 2188975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.6%; Score 2297; DB 1; Length 569; llarity 73.4%; Pred. No. 1.9e-46; Conservative 76; Mismatches 75; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-5,'A',7-15 <HUA>
Cross-references: UNIPARC:UP10000172DA8
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Best Local S:
Matches 416
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Length 569;

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A;Cross-references: UNIPARC:UPI00000C3801; GB:AP001507; GB:BA000004; NID:g10172612; PIDN:
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirs
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
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                                                                                                      SDSQAMGRAGEVIPRTWQTADKNKKEPGKLPEDGKDNDNFRIKRYISKYTINPALTHGVS 419
                                                        301 NPTRPYTINTLEEHLDMLMVCHHLDANIPEDIAFADSRIRKETIAAEDVLHDLGVFSMIS 360
                                                                                                                                                                                               EYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFG 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                          urease alpha subunit ureC [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSDSQAMGRAGEVIPRIWQTADKNKKEFGKLPED-GKDNDNFRIKRYISKYTINPALTHG
                                    TPTI PYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTS
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C,Superfamily: urease, alpha subunit; urease 62K chain homology
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                                                                                                                                                                                                                                                                                                                                        KTPEVFVDGKLCTSKPTSQVPLAQRYTFF
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A;Molecule type: DNA
A;Residues: 1-571 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TB-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Bacillus sp. C. C, Species: Bacillus sp. C. C, Species: Date: O'-Jul-1995 #text_change 05-Oct-2004 C;Date: O'-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 05-Oct-2004 C;Accession: C36950 B;Maeda, M.; Nakamura, A.; Masaki, H.; Uozumi, T. Bacteriol. 176, 432-442, 1994 Bacteriol. 176, 432-442, 1994 A;Title: Cloning, sequencing, and expression of thermophilic Bacillus sp. strain A;Reference number: A36950; MUID:94117379; PMID:8288539
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 AEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRANLKSM 182
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                                                      TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                                                                                                                                                                                                             GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
                                    LRAAEEYSMNVGFI,GKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                       VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
                                                                                                                                                                                                                                                  SQAMGRAGEVI PRTWQTADKNKKEFGKL,PEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                                                                                  IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      urease (BC 3.5.1.5) 61k chain - Bacillus sp. N,Alternate names: ureC protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-569 <MAE>
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Best Local S:
Matches 378
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Urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll1750
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75169
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Residues: 1-569 <KAN>
A, Cross-references: UNIPROT:P73061; UNIPARC:UP10000137D79; EMBL:D90903; GB:AB001339; NID:A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Superfamily: urease, alpha subunit; urease 62K chain homology
C;Keywords: hydrolase; metalloprotein; nickel
F;5-552/Domain: urease 62K chain homology <U62>
F;136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted
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                                                                                                                                                                                                                                                                                                                                     DVQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTT 300
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418 VSEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREM
                                                                                                                                                                                                                         PGHHGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITV
                                                                                  SSDSQAMGRAGEVIPRTWQTADKNKKEFGKLP-EDGKDNDNFRIKRYISKYTINPALTHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEAL
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A;Accession: S75169
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.8%; Score 1942; DB 2; Length 56
Best Local Similarity 62.6%; Pred. No. 6.3e-38;
Matches 356; Conservative 96; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    DPKTFEVFVDG-KL-CTSKPTSQVPLAQRYTFF
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Urease (alpha subunit) ureC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Cecesion: D69729
R;Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Broom, S.; Brouiller, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ebrlio, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Roningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
K; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Fark, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Saro, T.; Schroeter,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Tognoni, J.; Sekowska, A.; Seron,
A;Authors: Schleich, S.; Schroeter, R.; Yoshikawa, H.; Danchin, A.
A;Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Atters, Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Accession: D69729
A;Acteus number: A69580; MUID:98044033; PMID:9384377
A;Actus: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residuse: 1-569 -KUNA
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A;Experimental source: strain 168
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361 SSDSQAMGRVGEVIIRTWQTADKMKKQRGALAEDQGKGNDNVRIKRYVSKYTINPAITHG 420
                                                                                                                                                                    FGHHGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITV 537
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                                                     VSEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREM
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C;Superfamily: urease, alpha subunit; urease 62K chain homology
F;3-552/Domain: urease 62K chain homology <U62>
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A.Residues: 1-569 <MOE>
A,Residues: 1-569 <MOE>
A,Cross-references: UNIPROT:P41020, UNIPARC:UPI0000137D66, EMBL:X78411; NID:g498708, PIDACGenetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding DNA-fragment
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Keywords: heterodecamer; hydrolase; metalloprotein; nickel
F;3-552/Domain: urease 62K main homology 462,
F;136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted
                                       478
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                      419 AQYVGSVEAGKLADLCLWRPAFPGVKPEIVIKGGMIAWSQMGDANASIPTPQPVHMRPMF
                                                                                                     GSFAGARNATSLTFVSQAALEREIPQQLGLRKSAVAVSGTRQLTKQDMKLNDALPHIEVD
                                                                                                                                                                                                                                                                                                                                                                 #text_change 09-Jul-2004
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  SEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMF
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                                                                                                                                                                                                                                                                                                                                        C;Species: Bacillus pasteurii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_chang
C;Accession: S47104
R;Moersdorf, G.; Weinmann, P.; Kaltwasser, H.
submitted to the EMBL Data Library, June 1994
A;Description: Nucleotide sequence of three genes on a urease
A;Reference number: S47102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.4%; Score 1900; DB 2; Length 5 Best Local Similarity 59.1%; Pred. No. 6.4e-37; Matches 337; Conservative 112; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                       pasteurii
                                                                                                                                                             PKTFEVFVDGKLCTSKPTSQVPLAQRYTFF
                                                                                                                                                                                  urease (EC 3.5.1.5) 62K chain - Bacillus
N,Alternate names: ureC.protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S47104
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A;Start codon: GTG
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                                                                                                                                                                                                                                                                                                                                                                                                                   urease alpha chain [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004
C;Accession: AG2264
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-568 <KUR>
A;Cross-references: UNIPARC:UPI00000CE887; GB:BA000019; PIDN:BAB75369.1; PID:g17132803; A;Experimental source: strain PCC 7120
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                                                                                                                                       59 SPDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 ALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNL 178
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                                                                                                                                                                                                                        302 PTRPYTINTLEEHLDMLMVCHHLHRNIPEDVAFAESRIRRETIAAEDILHDLGAFSIISS
                                                            DSQAMGRVGEVICRTWQTAHKMKVQRGQLPGETG-NNDNLRAKRYVAKYTINPAITHGIS
                                                                                                                    EYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFG
                                                                                                                                                                                                 HHGKAKFDTSITFVSKVAYENGVKEKLGLEROVLPVKNCRNITKKDFKFNDKTAKITVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 A--DGAVDLVITNALILDWWGIVKADIGIKDGKIFKIGKAGNPYIQDHVD--IIIGPGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 EYDVQVAIHTDTI.NEAGFVEDTIAAFKORAIHTYHTEGAGGGHAPDIIKVCGQANVLPSS
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C;Superfamily: urease, alpha subunit; urease 62K chain homology
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                                                                                                                                                                                                                                                                                KTFEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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Riblischann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT: P44391; UNIPARC: UP10000137D6B; GB:U32736; GB:L42023; NID:g157; C;Superfamily: urease, alpha subunit; urease 62K chain homology C;Superfamily: urease for the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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                                                                                                                                                                                                                                                                          .Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
Accession: H64075
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                                                                                                                                                                      rease (EC 3.5.1.5) 62K chain - Haemophilus influenzae (strain Rd KW20);Alternate names: urease alpha chain
;Alternate names: urease alpha chain
;Species: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown; translation not shown
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       536 QVNPETYEVRVNGELVTCEPVDELPLAQKYFLF 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-572 <TIGR>
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                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                  C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Accession: C75586
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-568 <WHI>
A;Cross-references: UNIPARC:UPI0000C1687; GB:AE001863; GB:AE001825; NID:g6460670; PIDN:
A;Experimental source: strain Rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
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--PDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHRMLRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDH-CLSV 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSTTPTIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIA 356
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C;Superfamily: urease, alpha subunit; urease 62K chain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.7%; Score 1849; DB 2; Length 56 Best Local Similarity 59.2%; Pred. No. 1.1e-35; Matches 339; Conservative 100; Mismatches 124; Indela
                                                                                                                                                                                                                                                                                                                                                urease, alpha subunit - Deinococcus radiodurans (strain R1)
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                                                                                                                                          539 PKTFEVFVDGKLCTSKPTSQVPLAQRYTFF
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A,Cross-references: UNIPROT:P42885; UNIPARC:UPI000016FFCB; GB:S69145; NID:g545795; PIDN:; C;Genetics:
C;Genetics:
A;Gene: ureC
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Underson urea amidohydrolase; urease alpha chain; urease chain C
C,Species: Klebsiella pneumoniae
C,Species: Klebsiella pneumoniae
C;Bate: 30-Nov-1990 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
C;Accession: C36138
R;Mulrooney, S.B.; Hausinger, R.P.
J. Bacteriol. 172, 5837-5843, 1990
A,Title: Sequence of the Klebsiella aerogenes urease genes and evidence for accessory prodiction unber: A36138, MulD:91008957; PMID:2211515
Mol. Gen. Genet. 242, 539-550, 1994
A,Title: A 4.6 kb DNA region of Rhizobium meliloti involved in determining urease and
                                                                                                                                                                                                                                                                                                                                                                                                           predicted
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                                                                          A;Reference number: $42601; MUID:94166766; PMID:8121412
A;Accession: $42607
                                                                                                                                                                                                                                                                                                                    C;Superfamily: urease, alpha subunit; urease 62K cha C;Keywords: hydrolase; metalloprotein; nickel F;5-553/Domain: urease 62K chain homology <U62>F;136,138,219,362/Binding site: nickel 2 (His, His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTPEVPVDGKLCTSKPTSQVPLAQRYTPF 568
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A;Molecule type: DNA
A;Residues: 1-570 <MIK>
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                 urease alpha subunit PA4868 [imported] - Peeudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 06-Jan-2003
C;Accession: H83037
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83037
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;Residues: 1-566 <STO:
;Cross-references: UNIPARC:UPI00000C5E4A; GB:AE004900; GB:AE004091; NID:g9951134; PIDN:
;Experimental source: strain PAO!
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C;Species: Rhizobium meliloti
C;Species: S-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S42607
R;Miksch, G.; Arnold, W.; Lentzsch, P.; Priefer, U.B.; Puehler, A.
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                                                     Ridbri, E.; Karplus, P.A.

Submitted to the Brookhaven Protein Data Bank, June 1995

A; Reference number: A65977; PDB:IKRA

A; Contents: annotation; X-ray crystallography, 2.3 angstroms, residues 2-567

A; Title: The crystal structure of urease from Klebsiella aerogenes.

A; Ridbri, E.; Carr, M.B.; Hausinger, R.P.; Karplus, P.A.

Science 268, 998-1004, 1995

A; Title: The crystal structure of urease from Klebsiella aerogenes.

A; Reference number: A56340; MUID:95273988; PMID:7754395

A; Contents: annotation; X-ray crystallography, 2.3 angstroms

B; Contents: Structures of the Klebsiella aerogenes urease apoenzyme and two active-site mut

A; Title: Structures of the Klebsiella aerogenes urease apoenzyme and two active-site mut

A; Ritle: Structures of the Klebsiella aerogenes urease apoenzyme and two active-site mut

A; Contents: annotation; X-ray crystallography, 2.3 angstroms; active site mutagenesis
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A,Molecule type: DNA
A,Residues: 1-567 <MUL>
A,Cross-references: UNIPARC:UP100001120E5; GB:M36068; NID:g149335; PIDN:AAA25151.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                               Complex: trimer of heterotrimeric subunits consisting of 11K (gamma), 12K (beta), and
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A Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and two casportamily: urease, alpha subunit; urease 62K chain homology cycles, betractrimer; hydrolase; metalloprotein; nickel
7.4550/Domain: urease 62K chain homology vicks.
7.144,136,217,360/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted
7.217,246,272/Binding site: nickel 1 (Lys, His, His) #status predicted
7.217,186,272/Binding site: carbon dioxide (Lys) (covalent) (by urease activase) #status predicter
7.219,320/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-567 <JON>
A;Cross-references: UNIPROT:P17086; UNIPARC:UP10000137D74; GB:M31834; NID:g150914; PIDN:
          NiAlternate names: urease alpha chain
C;Species: Proteus mirabilis
C;Date: 03-Mar-1993 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
C;Accession: D43719
B;Jones, B.D.; Mobley, H.L.T.
J. Bacteriol. 177, 6414-6422, 1989
A;Title: Proteus mirabilis urease: nucleotide sequence determination and comparison with
A;Reference number: A43719; MUID:90078080; PMID:2687233
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mirabilis
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539 QTYIVKADGVPLVC--EPATELPMAQRYFLF 567
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R;Moersdorf, G.; Kaltwasser, H.
FEMS Microbiol. Lett. 66, 67-74, 1991
A;Title: Cloning of the genes encoding urease from Proteus vulgaris and sequencing of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and tw C; Superfamily; urease, alpha subunit; urease 62K chain homology C; Keywords: heterotrimer; hydrolase; metalloprotein; nickel C; Keywords: heterotrimer; hydrolase; metalloprotein; nickel F; 4-550/Domain: urease 62K chain homology < (62>)
F; 134, 136, 217, 160/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted F; 217, 246, 272/Binding site: nickel 1 (Lys, His, His) #status predicted F; 217, 181 site: carbon dioxide (Lys) (covalent) (by urease activase) #status predict F; 219, 320/Active site: His #status predicted
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: ureC
C;Complex: trimer of heterotrimeric subunits consisting of 11K (gamma), 12K (beta), and
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                                                                                                                                                                                                                           C;Date: 29-Jan-1993 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
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539 QTYIVKADGVPLVC--EPATELPMAQRYFLF 567
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                                                                                                                                      urease (EC 3.5.1.5) 62K chain - Proteus vulgaris
                                                                                                                                                                 N,Alternate names: urease alpha chain
C,Species: Proteus vulgaris
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A;Residues: 1-567 <MOE>
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

August 9, 2006, 21:34:37; Search time 305 Seconds

(without alignments) 1722.652 Million cell updates/sec

US-09-904-994B-3 2999

Title: Perfect score:

1 MKMKKQEYVNTYGPTKGDKV.....KLCTSKPTSQVPLAQRYTFF Sequence:

568

BLOSUM62 Scoring table:

Gapop 4.0 , Gapext 1.0

2849598 seqs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q8gh97 helicobacte	P42823 helicobacte	Q7x3w5 helicobacte	P69997 helicobacte	P69996 helicobacte		Q38q64 helicobacte	_		Q84f75 helicobacte		-	Q93pj4 helicobacte	_		-	P77837 bacillus su	Q4che3 clostridium	052305 synechococc		Q2zgt0 caldicellul		Q733j6 bacillus ce	Q8dmv6 synechococc	Q3fba4 burkholderi	Q454ml burkholderi	Q41nh4 burkholderi	Q5fb23 campylobact			
SUMMAKIES	ID	ОВСН97 НЕГВІ	URE2 HELHE	Q7X3W5 HELPY	URE2 HELPJ	URE2 HELPY	Q9S0QS_HELPY	Q38Q64_HELPY	Q64EY3 HELPY	Q9AFB1 HELPY	Q84F75_HELPY	Q8RNU6_HELPY	URE2_HELFE	Q93PJ4 HELHP	URE1_BACSB	Q9KG59_BACHD	QSKYM1_GEOKA	URE1 BACSU	Q4CHE3 CLOTM	052305_SYNP2	URE1_SYNY3	Q2ZGT0_CALSA	Q3M712_ANAVT	Q733J6_BACC1	Q8DMV6 SYNEL	Q3FBA4_9BURK	Q454M1 9BURK	04LNH4 9BURK	Q5FB23_CAMLA	Q48DE6_PSE14	Q87VP0 PSESM	Q4ZN06_PSEU2
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ap (Match	77.6	76.8	76.7	9.92	9.9/	9.92	76.5	76.4	76.4	76.3	75.1	74.8	70.3	68.2	67.6	66.7	9.99	66.2	65.7	64.8	64.8	64.4	64.4	64.4	64.3	64.2	64.2	64.2	64.1	64.1	64.0
	Score	2326	2304	2301	2297	2297	2297	2293	2292	2291	2288	2251	2244	2109	2044	2027	1999	1998	1986	1971	1942	1942	1932	1932	1930	1929	1926	1926	1924	1921	1921	1920
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Q391W3_BURS3 Q8YQZQ_ANASP Q461Y3_PROWT Q481H6_BURV1 Q3KTZ_PSEPP Q34XKG_9GAM G65RL3_BURPS Q2UQ88_GCYAN Q4KX10_PSEPF Q62HSO_BURNA Q62HSO_BURNA Q4XY10_PSEPF	URE1_BACPA Q3WT92_9RHIZ
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ALIGNMENTS

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62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMODGVSPHMVVGVGTEALA 121
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                                                                                                                                          Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter:
                                                                                                                                                                                                                                    MEDLINE=22540228; PubMed=12652903; DOI=10.1080/1042517021000039230; Zhu J., Teng C.F., Chang C.F., Chang C.F., Chang C.F., McDonough B., McDonough S., McDonough S., McConough T., Teng Y.F., McCloning and characterization of a Helicobacter bizzozeronii urease
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R GO; GO: 0016151; F: nickel ion binding; IEA.

R GO; GO: 0016151; F: nickel ion binding; IEA.

R GO; GO: 0019657; F: urease activity; IEA.

R GO; GO: 0019657; F: urease activity; IEA.

R InterPro; IPR006680; Amidohydrol.

R InterPro; IPR0068029; Urease alpha.

R InterPro; IPR008295; Urease alpha.

R PEan; PF01979; Amidohydroli.

R PEAN; PF01979; Amidohydroli.

R PERSF; PIRSF001226; Urease alpha; 1.

R PRRSF; PIRSF001226; Urease alpha; 1.

R PRINTS; PR01752; UREASE.

R TIGRFAMS; TIGR01792; urease alph; 1.

R PROSITE; PS01120; UREASE 1; 1.

R PROSITE; PS01120; UREASE 2; 1.
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                                                 01-MAR-2003, integrated into UniProtKB/TrEMBL.
             569 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF330621; AA015374.1; -; Genomic_DNA.
             PRT;
                                                                     01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 14.
             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       gene cluster.";
DNA Seq. 13:321-331(2002).
                                                                                                                           Helicobacter bizzozeronii.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=9422523; PubMed=8168924;

MEDLINE=9422523; PubMed=8168924;

A Solnick J.V., O'Rourke J., Lee A., Tompkins L.S.;

Molecular analysis of urease genes from a newly identified uncultured species of Helicobacter.;

In fect. Immun. 62:1631-1638(1994).

--- CATALTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).

--- CATALTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).

--- CATALTIC Consists of two subunits (alpha and beta).

--- SUBUNIT: Consists of two subunits (alpha and beta).

--- FTW: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (by similarity).

--- FTW: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (by similarity).

--- SIMILARITY: Belongs to the urease family.

--- CAUTION: In Helicobacter the beta subunit is what is known in other bacteria as the alpha subunit.
                                                                 243 VQVAIHTDTLNEAGCVEDTLQAIAGRTIHTFHTEGAGGGHAPDVIKASGEFNILPASTNP
                                                                                                                                           TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                       GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM
                                                     LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                VQVCIHTDTVNEAGYVDDTL.NAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
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Helicobacteraceae; Helicobacter.
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InterPro; IPR001848; Urease alpha.
InterPro; IPR011612; Urease alpha N.
InterPro; IPR008295; Urease_alphaIone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRAABEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYKKOEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                           /FIGENCO (BY SIMILATIV).
Proton donor (By Similarity).
Nickel 2 (By Similarity).
Nickel 1 (By Similarity).
Nickel 1 (By Similarity).
Nickel 1 (By Similarity).
Nickel 1 (By Similarity).
Nickel 1 (By Similarity).
Nickel 1 (By Similarity).
Nickel 1 (By Similarity).
Substrate (By Similarity).
Substrate (By Similarity).
W, E2C036DF30377917 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                            76.8%; Score 2304; DB 1;
llarity 73.7%; Pred. No. 1.1e-42;
Conservative 74; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrated into UniProtKB/TrEMBL
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Pfam; PF01979; Amidohydro_1; 1.
Pfam; PP00449; Urease_alpha; 1.
PIRSF; PIRSF00125; Urease_alpha; 1.
PRINTS; PR01752; UREASE.
TIGREAM; TIGR01792; urease_alph; 1.
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS00145; UREASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEVFVDGKLCTSKPTSQVPLAQRYTFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 YKVKVDGNEVTSHAADKLSLAQLYNLF
                                                                                                                                                                   Urease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence version 1. entry version 12.
                                                                                                                                          Hydrolase; Metal-binding; Nickel
CHAIN 1 568 Urea
                                                                                                                                                                                                                                                                                                                                                                                      61870 MW;
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136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 VQVAIHTDTLNEAGCVEDTWAAIAGRTWHTFHTEGAGGGAAPDIIKVAGEHNILPASTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIPFIVNTEAEHMDMLMVCHHLDKSIKEDVQPADSRIRPQTIAAEDTLHDMGIFSITSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KWKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRAAEEYSMINVGFLGKGINSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGGHSPDVITMAGELNILPSSTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                     Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                           Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                 75; Indels
                                                                                        STRAIN=MEL-HP27;
Duan G.C., Dai L.P.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1752; UREASE. TIGREAMS; TIGREAMS; TIGRO1792; UREASE alph; 1. PROSITE; PSO1120; UREASE 1; 1. PROSITE; PSO10145; UREASE 2; 1. SEQUENCE 569 AA; 61671 MW; 4C96852826C7A784 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          76.7%; Score 2301; DB 2; 73.5%; Pred. No. 1.3e-42;
                                                                                                                                                                                        GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0019039; F:urease activity; IEA.
GO; GO:0019627; P:urea metabolism; IEA.
INTERPO; IPR006680; Amidohydro I.
INTERPO; IPR001612; Urease alpha.
INTERPO; IPR011612; Urease alpha.
INTERPO; IPR010612; Urease alpha.
INTERPO; IPR010612; Urease alpha N.
INTERPO; IPR010612; Urease alpha N.
INTERPO; IPR010612; Urease alpha N.
INTERPO; IPR010612; Urease alpha N.
INTERPO; IPR010612; Urease alpha N.
INTERPO; IPR010612; Urease alpha N.
INTERPO; IPR010612; Urease alpha N.
INTERPO; IPR010612; Urease alpha N.
INTERPO; IPR010612; Urease alpha N.
                                                                                                                                                                    EMBL; AY295085; AAP51176.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                               75; Mismatches
                                                                                                                                                                                                                                                                                                        PIRSF; PIRSF001226; Urease_alpha; 1.
                                           Helicobacteraceae; Helicobacter.
NCBL_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 417; Conservative
                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                   P14917; 1E9Y
Trease B.
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [L.S.L., Mois D.T., King B.L., Brown E.D., Doig P.C.,
Alm R.A., Ling L.-S.L., Mois D.T., King B.L., Carmel G.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
                                                                                                                                                                                                                                                  P69957; P14917;
04-JJN-2005, integrated into UniProtKB/Swiss-Prot.
04-JJN-2005, sequence version 1.
07-MAR-2006, entry version 7.
Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase).
Name=ureB; Synonymas=hpuB; OrderedLocusNames=uFH90067;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).

-!- PTM: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).
-!- MISCELLANBOUS: Oligomerization may protect the enzyme against denaturation in an acidic environment (By similarity).
-!- SIMILARITY: Belongs to the urease family.
-!- CAUTION: In Helicobacter the beta subunit is what is known in other bacteria as the alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-i- COFACTOR: Binds 2 nickel ions per subunit (89 similarity).
-i- SUBUNIT: Heterohexamer of 3 alpha and 3 beta subunits. Four heterohexamers assemble to form a 16 nm spherical complex (8y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proton donor (By similarity).
Nickel 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
Nickel 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
Nickel 2 (By similarity).
Nickel 2 (By similarity).
Nickel 2 (By similarity).
Substrate (By similarity).
W, 4C8A6BC6C8295584 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urease beta subunit.
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PIR; B38537; URKCBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenomeReviews; AE001439 GR; JHP0067.
InterPro; IPR005680; Amidohydro 1.
InterPro; IPR005848; Urease alpha.
InterPro; IPR0011612; Urease alpha N.
InterPro; IPR008295; Urease alpha N.
Pfam; PF01979; Amidohydro 1; 1.
Pfam; PF04499; Urease alpha; 1.
PIRRF; PIRSF001226; Urease alpha; 1.
TIGRPAM; PG0792; UREASE.
TIGRPAM; PG07979; UREASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                     : |||||| |||| :: ||| :: |
543 YHVFVDGKEVTSKPATKVSLAQLFSIF
542 FEVFVDGKLCTSKPTSQVPLAQRYTFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacteraceae; Helicobacter
NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01120; UREASE 1; 1. PROSITE; PS00145; UREASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61684 MW;
                                                                                                                                                                                                                                 STANDARD;
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274
362
221
569 AA;
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                                                                                                                                                                                                                                                                                                                                                   62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                                                                                                  GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKMNLHRM 181
                                                                                                                                                                                          VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 301
                                                      Labigne A., Cussac V., Courcoux P.; "Shuttle cloning and nucleotide sequences of Helicobacter pylori genes responsible for urease activity."; J. Bacteriol. 173:1920-1931(1991).
                                                                                                                                                                SQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY
                                           KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGOSNSPD
                                                                                                                                                       LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                  SQAMGRAGEVIPRIWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                                                                                                                      IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90221820; PubMed=2326167;
Clayton C.L., Pallen M.J., Kleanthous H., Wren B.W., Tabaqchali S.;
"Nucleotide sequence of two genes from Helicobacter pylori encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                         ö
      76.6%; Score 2297; DB 1; Length 5 73.4%; Pred. No. 1.6e-42; Live 76; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          UREZ HELPY STANDARD; PRT; 569 AA.
P69996; P14917; Q9R3B3;
04-JAN-2005, integrated into UniProtxB/Swiss-Prot.
04-JAN-2006, equence version 1.
07-MAR-2006, entry version 11.
Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase).
Name=ureB; Synonyms=hpus; OrderedLocusNames=HP0072;
                                                                                                                                                                                                                                                                                                                                                                                         FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=85P; PubMed=2001995; MEDLINE=91161505; PubMed=2001995;
              Best_Local Similarity /3.*
Matches 416; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=210;
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STRAIN-26695 / ATCC 700392;

WEDLINE-9739467; PubMed=9252185; DOI=10.1038/41483;

Tomb J.-F., White O., Kerlavage A.C., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,

Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F.,

Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F.,

Beterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,

Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,

Hickey B.K., Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D.,

Kalley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,

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Smith H.O., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE OF 1-30, AND KINETIC PARAMETERS.
PubMed=1857197; DOI=10.1016/0882-4010(91)90062-F;
Evans D.J. Jr., Evans D.G., Kirkpatrick S.S., Graham D.Y.,
"Characterization of the Helicobacter pylori urease and purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cussac V., Ferrero R.L., Labigne A.; "Expression of Helicobacter pylori urease genes in Escherichia coli grown under nitrogen-limiting conditions.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimum pH is 8.0. Active from pH 4.0 to 10.0; SUBUNIT: Heterohexamer of 3 alpha and 3 beta subunits. Four heterohexamers assemble to form a 16 nm spherical complex. PTM: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 1-15.

BEGILINE-2002165. PubMed=2318539;
Hu L.T., Mobley H.L.T.;
"Purification and N-terminal analysis of urease from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn B.E., Campbell G.P., Perez-Perez G.I., Blaser M.J.; "Purification and characterization of urease from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS), AND SUBUNIT STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
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-! CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- COFACTOR: Binds 2 nickel ions per subunit.
-!- BIOPHYSICOCHEMICAL PROPERTIES:
                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                 Nucleic Acids Res. 18:362-362(1990)
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Biol. Chem. 265:9464-9469(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90264448; PubMed=2188975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infect. Immun. 58:992-998(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pylori.";
Nature 388:539-547(1997).
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urease subunits.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of its subunits.";
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J. Biol.
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ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GEGLIVTAGGIDTHIHFISPQOIPTAFASGVTTMIGGGTGPADGTNATTITFGRRNLKWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 IRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKCHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSOSRIRPGSIAAEDVLHDMGVIAMTSSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.6%; Score 2297; DB 1; Length 5 73.4%; Pred. No. 1.6e-42; rative 76; Mismatches 75; Indels
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    Similarity
    62
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InterPro; IPR006848; Urease_alpha.

InterPro; IPR0083848; Urease_alpha.

InterPro; IPR008395; Urease_alpha.

InterPro; IPR008395; Urease_alpha.

InterPro; IPR008395; Urease_alpha.

InterPro; IPR008395; Urease_alpha; 1.

InterPro; IPR00849; Urease_alpha; 1.

INTERPAMS; ITGR01205; UREASE.

INTERPAMS; ITGR01205; UREASE.

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Distributed under the Creative Commons Attribution-NoDerivs License
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-I- MISCELLANEOUS: Oligomerization may protect the enzyme against denaturation in an acidic environment.
-I- SIMILARITY: Belongs to the urease family.
-I- CAUTION: In Helicobacter the beta subunit is what is known in other bacteria as the alpha subunit.
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Nickel 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
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EMBL; X17079; CAA34933.1; -; Genomic DNA.
EMBL; A08818; CAA00811.1; -; Unassigned DNA.
EMBL; A07399; CAA00663.1; -; Unassigned DNA.
EMBL; A8005511; AAD07143.1; -; Genomic DNA.
EMBL; M84338; -; NOT ANNOTATED CDS; Genomic DNA.
PIR; B38537; URKCBP.
PDB; 1E9Y; X-ray; B=1-569.
GenomeReviews; AE000511_GR; HP0072.
TIGR; HP0072; -.
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LRAABEYSMNVGFLGKGNSSSKKQLVRQVBAGAIGFKLHEDWGTTPSAIDHCLSVADEYD 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KISRKEYASMYGPITGDKVRLGDTDLIAEVEHDYTIYGEELKFGGGKTLREGMSQSNNPS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                         182 IRAABEYSMNIGFLAKGNASNDASLADQIEAGAIGFKIHEDWGTTPSAINHALDVADKYD
                                                                                                                                                                                             GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
                                        363 SOAMGRVGEVITRTWOTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPALAHGISEY
                                                                                             422 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Urease B (Fragment).
Helicobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.5%; Score 2293; DB 2; Length 5 73.2%; Pred. No. 2e-42; ive 76; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li Y., Ning Y.-S., Long M., Wang Y.-D., Dong W.-Q., Li M. Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 AA; 61524 MW; 5CD9DC062D41F883 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-2005, integrated into UniProtKB/TrEMBL. 22-NOV-2005, sequence version 1. 07-FEB-2006, entry version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, D0141576; ABA87133.1; -; Genomic DNA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0019627; F:ureas activity; IEA.
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543 YHVFVDGKEVTSKPATKVSLAQLFSIF 569
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
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                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20305050; PubMed=10844692; MEDLINE-20305050; PubMed=10844692; Akada J.K., Shirai M., Takeuchi H., Tsuda M., Nakazawa T.; Akada J.K., Shirai M., Takeuchi H., Tsuda M., Nakazawa T.; "Identification of the urease operon in Helicobacter pylori and its control by mRNA decay in response to pH.";
                                                                                                                                                                                                                                        Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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73.4%; Pred. No. 1.6e-42;
tive 76; Mismatches 75; Indels
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                                                                                                               01-MAY-2000, integrated into UniProtKB/TrEMBL
01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:001617; F:hydrolase activity; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0016015; F:nickel ion binding; IEA.
GO; GO:00109029; F:urease activity; IEA.
GO; GO:0019627; P:urea metabolism; IEA.
InterPro; IPR005848; Urease alpha.
InterPro; IPR011612; Urease alpha.
InterPro; IPR011612; Urease alpha.
InterPro; IPR011612; Urease alpha.
InterPro; IPR01162; Urease alpha.
Ffam; PF01479; Amidohydro 1; IPR01175; Urease alpha; IPPRNTS; PR01752; UREASE.
IGRFAMS; TIGRTON172; UREASE.
IGRFAMS; TIGRTON172; UREASE.
IGRFAMS; TIGRTON172; UREASE.
IPROSITE; PS01120; UREASE.
IPROSITE; PS01120; UREASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB032429; BAA84533.1; -; Genomic_DNA
HSSP; P14917; 1E9Y.
                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=210;
                                                                    Q9S0Q5_HELPY
Q9S0Q5;
                                                                                                                                                                                                                       Name=ureB;
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EGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRML 182
                                                                     242 QVAIHTDTLNEAGCVEDTWAAIAGRTWHTFHTEGAGGGHAPDIIKVAGEHNILPASTNPT 301
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                                                                                                                                                                                                                                                                                                                 363 QAMGRAGEVIPRIWQTADKNKKEFCKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEYI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                  QUCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTPT
                                                                                                                                                                                                                                                  303 IPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSDS
                                                                                                                                                                                                                                                                                                                                                                                 423 GSVEEGKIADLVVWNPAFFGVXPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 KAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKTF
                                                                                                                   RAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGPKLHEDWGTTPSAIDHCLSVADEYDV
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerold A., Simpson K., Chang Y.-F.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
01-00N-2001, integrated into UniProtKB/TrEMBL. 01-0UN-2001, sequence version 1. 07-FEB-2006, entry version 20.
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GO; GO:0016781; F:hydrolase activity; IEBA.

GO; GO:0016151; F:nickel ion binding; IEBA.

GO; GO:0009039; F:urease activity; IEBA.

GO; GO:0019627; P:urease activity; IEBA.

InterPro; IPRO06880; Amidohydro_1.

InterPro; IPRO06888; Urease_alpha.

InterPro; IPRO08181; Urease_alpha.

InterPro; IPRO08295; Urease_alpha.

Ffam; PF01979; Amidohydro_1; I.

Pfam; PF01979; Amidohydro_1; I.

Pfam; PR01752; UREASE.

PRINTS; PR01752; UREASE.

TIGRFAM8; TIGRFAN192; urease_alpha; I.

PROSITE; PS01120; UREASE.

PROSITE; PS01120; UREASE_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF352376; AAK32714.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 EVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 HVFVDGKEVTSKPATKVSLAQLFSIF
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SQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY 421
                                                                                                                                  IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH 481
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                                                                                                                                                                                  GKAKFDTSITFVSKVAYENGVKEKL, GLEROVL PVKNCRNITKKD FKFNDKTAKITVDPKT
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                                                 SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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"Construction of prokaryotic expression system of ureB gene from
clinical Helicobacter pylori strain and identification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61444 MW; 1DFA1AA596205A9C CRC64;
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25-OCT-2004, sequence version 1.
07-FBB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY714224; AAU21200.1; -; Genomic_DNA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016151; F:hydrolase activity; IEA.
GO; GO:0009039; F:urease activity; IEA.
GO; GO:0019627; P:urea metabolism; IEA.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR00848; Urease_alpha N.
InterPro; IPR008295; Urease_alpha N.
InterPro; IPR008295; Urease_alpha N.
PIMEP; PIRSF01979; Amidohydro_1; 1.
Pfam; PF00449; Urease_alpha; 1.
PIRSF; PIRSF01225; Urease_alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant protein immunity."; World J. Gastroenterol. 10:977-984(2004).
                                                                                                                                                                                                                                                  542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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542 YHVFVDGKEVTSKPANKVSLAQLFSIF 568
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TIGREAMS; TIGR01792; urease alph; 1.
PROSITE; PS001120; UREASE 1; 1.
PROSITE; PS00145; UREASE 2; 1.
SEQUENCE 567 AA; 61444 WM; 1DPA1
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Matches 415; Conservative
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NUCLEOTIDE SEQUENCE.
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064EY3;
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                                                                                                                                                                                                                               VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTTP 301
                                                                                                                                                                                                                                                                        TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD 361
                                                             2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD 61
                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                  SOAMGRAGEVIPRTWOTADKNKKEFGKLPEDGKONDNFRIKRYISKYTINPALTHGVSEY
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                                         Gaps
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Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                   Length 569;
                   Query Match 76.4%; Score 2291; DB 2; Length 5 Best Local Similarity 73.2%; Pred. No. 2.2e-42; Matches 415; Conservative 76; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karimi Arzenani M., Mohammadi M.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
C243ABC38C25D187 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q84F75 HELPY PRELIMINARY; PRT; 569 AA. 084F75. 01-UN-2003, integrated into UniProtKB/TrEMBL. 01-UN-2003, sequence version 1. 07-FBB-2006, entry version 13. Urease beta (EC 3.5.1.5).
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HSSP; P14917; 1E9Y.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
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61714 MW;
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569 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.3%; Score 2288; DB 2; Length 5 Best Local Similarity 73.2%; Pred. No. 2.6e-42; Matches 415; Conservative 75; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                               569 AA; 61698 MW; D35279ED45EF712F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002, integrated into UniProtKB/TrEWBL. 01-JUN-2002, sequence version 1. 07-FBB-2006, entry version 16. Urease B subunit.
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GO; GO:0009039; F:urease activity; IEA.
GO; GO:0019627; P:urea metabolism; IEA.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR001612; Urease_alpha.
InterPro; IPR001612; Urease_alpha.
InterPro; IPR008295; Urease_alpha.
Ffam; FP01979; Amidohydro_1; 1.
Ffam; FP01979; Amidohydro_1; 1.
PIRSF; PIRSF001226; Urease_alpha; 1.
PIRSF; PRRF001226; Urease_alpha; 1.
PROSITE; PS001120; UREASE_I; 1.
PROSITE; PS001120; UREASE_I; 1.
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363 SQAMGRVGEVITRTMQTADKOKKEFGRLKEEKGDNDNPRIKRYLSKYTINPAIAHGISEY 422
                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                          IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter felis.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Turbett G.R., Hoej P.B., Horne R., Mee B.J.;

Purification and characterization of the urease enzymes of Helicobacter species from humans and animals.";

Infect. Immun. 60:5259-566(199).

-!- CATALYTIC ACTIVITY: Urea + H(2)0 = CO(2) + 2 NH(3).

-!- CATALYTIC ACTIVITY: Urea + H(2)0 = CO(2) + 2 NH(3).

-!- SUBUNIT: Consists of two subunits (alpha and beta).

-!- PTW: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).

-!- SIMILARITY: Belongs to the urease family.

-!- CAUXION: In Helicobacter the beta subunit is what is known in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94018627; PubMed=8412683;
Ferrero R.L., Labigne A.;
"Cloning, expression and sequencing of Helicobacter felis urease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIRSF; PIRSP001226; Urease_alpha; 1.
PRINTS; PR01752; UREASE.
TIGRFAMS; TIGR01792; urease_alph; 1.
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS0145; UREASE 2; 1.
Object protein sequencing; Hydrolase; Metal-binding; Nickel.
CHAIN 1 569
                                                                                                                                                                                                                                                                                                                                    Q087<u>T6; Q9R3B3;</u>
01-OCT-1994, integrated into UniProtKB/Swiss-Prot.
01-OCT-1994, sequence version 1.
07-FEB-2006, entry version 47.
Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase)
                                                                                                                                                                                                                                                                                                                         569 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X69080; CAA48826.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other bacteria as the alpha subunit.
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PIR; S3521; S32291.
RSSP; P14917; 1892.
InterPro; IPR006680; Amidohydro 1.
InterPro; IPR005848; Urease_alpha.
InterPro; IPR01612; Urease_alpha.
InterPro; IPR01612; Urease_alpha.
Pitarpro; IPR01825; Urease_alpha.
Pfam; PF01979; Amidohydro 1; 1.
Pfam; PF0449; Urease_alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Microbiol. 9:323-333(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 1-12.
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543 YHVFVDGKEVT 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                        Opazo P., Muller I., Rollan A., Valenzuela P., Yudelevich A.,
Garcia-de la Guarda R., Urra S., Venegas A.;
"Serological response to Helicobacter pylori recombinant antigens in
Chilean infected patients with duodenal ulcer, non-ulcer dyspepsia and
gastric cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 LRAABEYSMNLGFLAKGNASNDASLADQIBAGAIGFKIHEDWGTTPSAINHALDVADKYD
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                                                                                                                                                                                                                                               MEDLINE=22121498; PubMed=12125208; Muller I., Medina-Selby A., Palacios J.L., Martinez P., Opazo P., Bruce B., Mancilla M., Valenzuela P., Yudelevich A., Venegas A.; "Cloning and comparison of ten gene sequences of a Chilean H. pylori strain with other H. pylori strains revealed higher variability for VacA and CagA virulence factors."; Biol. Res. 35:67-84(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF479026; AAL86896.1; -; Genomic_DNA.
HSSP; P14917; 1E9Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0009039; F:urease activity; IEA.
GO; GO:0019627; F:urea metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006680; Amidohydro 1.
InterPro; IPR005848; Urease_alpha.
InterPro; IPR001612; Urease_alpha.
InterPro; IPR008295; Urease_alpha N.
Pfam; PF01979; Amidohydro 1; 1.
Pfam; PF0449; Urease_alpha; 1.
Pfam; PF00449; Urease_alpha; 1.
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TIGREPANS; TIGR01792; urease alph; 1.
PROSTIE; PS01120; UREASE 1; 1.
PROSTIE; PS00145; UREASE 2; 1.
                                                                         MEDLINE=20123532; PubMed=10660136;
                                                                                                                                                                              APMIS 107:1069-1078(1999)
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   NCBI_TaxID=210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 VQVAIHTDTLMBAGCVEDTLEAIAGRTIHTFHTEGAGGGHAPDVIKWAGEFNILPASTNP 302
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Helicobacteraceae, Helicobacter.
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                                                                                                                                                                                                              74.8%; Score 2244; DB 1; Length 569; 72.5%; Pred. No. 2.5e-41; ive 71; Mismatches 85; Indels
             Proton donor (By similarity).
Nickel 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
Nickel 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
Nickel 2 (By similarity).
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Substrate (By similarity).
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MEDLINE=21391860; PubMed=11500473;
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61703 MW;
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Matches 411; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
DOI=10.1128/IAI.69.9.5914-5920.2001;
Beckwith C.S., McGee D.J., Mobley H.L.T., Riley L.K.;
"Cloning, expression, and catalytic activity of Helicobacter hepaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 YTNELDAVITNAMIIDYTGIYKADIGIKGGKIVGIGKAGNPDTQDSVNEAMVVGAATEVI
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                                                                                                                                                                                                                                                                         STRAIN=ATCC 51449 / 3B1;
MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
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RIGO; GO:0016797; F:hydrolase activity; IEA.
RIGO; GO:0016121; F:nickel ion binding; IEA.
RIGO; GO:00106121; F:urease activity; IEA.
RIGO; GO:0019627; F:urease activity; IEA.
RIGO; GO:0019627; F:urease activity; IEA.
RIGO; GO:0019627; F:urease activity; IEA.
RIGORDOSA84; Urease alpha.
RIGORDOSA94; Urease alpha.
RIGORDOSA95; Urease alpha.
RIGORDOSA95; Urease alpha; 1.
RIGORDOSA95; Urease alpha; 1.
RIGORDOSA95; Urease alpha; 1.
RIGORDOSA95; Urease alpha; 1.
RIGORDOSA95; UREASE.
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RROSITE; PS01120; UREASE.
RROSITE; PS01120; UREASE.
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RROSITE; PS01140; UREASE.
RROSITE; PS01140; UREASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter hepaticus.";
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
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68.1%; Pred. No. 2.8e-38;
ive 83; Mismatches 95;
                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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EMBL; AE017125; AAP77005.1; -; Genomic_DNA.
HSSP; P18314; 1ASN.
HSSP; P18314; 1ASN.
                                                                                                                                                             Infect. Immun. 69:5914-5920(2001)
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Best Local Similarity 68.1
Matches 388; Conservative
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DSQAMGRVGEVITRTWQTADKCKNEFGALKEECG-ENDNFRIKRYISKYTINPAIAHGIS 420
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                                                                                                                    481 SYGKAKYNCAITFVSKIAYDCHIKEELGIERILLPVKNCRNITKKDMKFNDVITPIEVNP
                                                  HIGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDP
                                 EYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUCLEOTIDE SEQUENCE [GENOMIC DNA], AND PARTIAL PROTEIN SEQUENCE.
MEDLINE=94117379; Pubmed=828839;
Macda M., Hadaka M., Nakamura A., Masaki H., Uozumi T.;
Macda M., Hadaka M., Nakamura A., Masaki H., Uozumi T.;
Macda M., Nakamura A., Masaki H., Uozumi T.;
Gloning, sequencing, and expression of thermophilic Bacillus sp.
strain TB-90 urease gene complex in Bscherichia coli.";
J. Bacteriol. 176;432-442[1994].
GARALYIIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
COPACTOR: Binds 2 nickel ions per subunit (By similarity).
SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).
SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).
Hym: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D14439; BAA03325.1; -; Genomic_DNA.

R HSSP; P18134; IBAA03325.1; -; Genomic_DNA.

R HSSP; P181314; IBSTA.

InterPro; IPR010550; Amidohydro_like.

R InterPro; IPR011550; Amidohydro_like.

R InterPro; IPR011612; Urease_alpha.

R InterPro; IPR00295; Urease_alpha.

R Pfam; PF01979; Amidohydro_l; 1.

R Pfam; PF01979; Amidohydro_l; 1.

R PRSP; PRRSP001226; Urease_alpha; 1.

R PRNTS; PR01752; UREASE.

R ProDom; PD001248; Amidohydro_like; 1.

R PTGRPAM; TIGRO1792; urease_lph; 1.

R PROSITE; PS001120; UREASE_1; 1.

R PROSITE; PS001120; UREASE_2; 1.

R PROSITE; PS001130; UREASE_2; 1.

R PROSITE; PS001130; UREASE_2; 1.

R PROSITE; PS001130; UREASE_2; 1.

R PROSITE; PS001130; UREASE_2; 1.

R PROSITE; PS001130; UREASE_2; 1.

R PROSITE; PS001145; UREASE_2; 1.

R PROSITE; PS001145; UREASE_2; 1.

R PROSITE; PS001145; UREASE_2; 1.

R PROSITE; PS001145; UREASE_2; 1.

R PROSITE; PS001145; UREASE_2; 1.

R PROSITE; PS001145; UREASE_2; 1.

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R PROSITE; PS001145; UREASE_2; 1.

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R PROSITE; PS001145; UREASE_2; 1.
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Nickel 2 (By similarity).
Substrate (By similarity).
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=36824;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                             3 MKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQ---SNS
                                                                                                                                      RMLRAABEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADE
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                                                         Gaps
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                                                         7;
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui P., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
     Length 569;
  68.2%; Score 2044; DB 1; Length 5 66.4%; Pred. No. 8.1e-37; Live 76; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-077-2000, integrated into UniProtKB/TrEMBL 01-077-2000, sequence version 1. 07-FEB-2006, entry version 25. Urease alpha subunit (BC 3.5.1.5).
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                              Best Local Similarity bb.41
Matches 378; Conservative
Query Match
Best Local Similarity
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Q9KG59;
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59 SPDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTE 118
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SEQUENCE 571 AA; 61292 MW; 397398DECEA0ABOF CRC64;
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PIR; F83681; F83681.

HSSP; P41020; 1UBP.

SMR; Q9KG59; 1-571.

BioCyc; BHAL6665:BH0254-MONOMER; -.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:001627; F:ureas activity; IEA.

GO; GO:0019627; F:ureas activity; IEA.

INTERPO: IPRO06680; Amidohydro 1.

INTERPO: IPRO0899; Verase alpha N.

INTERPO: IPRO08295; Urease alpha N.

PEAM; PF01979; Amidohydro 1.

PEAM; PF01979; Amidohydro 1.

PEAM; PF01979; MIGANSE.

INTERPO: IRRSF001226; Urease alpha; 1.

PROSITE; PS01120; URRASE.

INGRAMS; TIGRO1792; urease alph; 1.

PROSITE; PS01120; URRASE.

INTERPORTE: PS01120; URRASE.

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Search completed: August 9, 2006, 21:43:01 Job time : 309 secs

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9, 2006, 13:30:32; Search time 194 Seconds (without alignments) 615.121 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* geneseqp2005s:* geneseqp2002s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

	Description	Aec92007 Single ch	Adw24449 HCMV-Fab-	Adu04216 Human imm	Aae35907 Human A17	Abo27142 Human ger	Adf10189 Antibody	Adf10087 VEGF anti		Adj80262 Vkappa ge	Human a	Ady75436 Human ger		Aeb13642 Human var	Aed04308 Human ant	Aed06937 Human ant	Aee47598 Human CDR	Aef18501 HAHA prot	Aae06948 Human HF-	Aae06996 Human kap	Aau09920 Human ant	Abr61476 Human ant	Adq89233 Human imm	Adq89281 Human imm
SUMMARIES	рв ір	9 AEC92007	8 ADW24449	8 ADU04216	6 AAE35907	6 ABO27142	7 ADF10189	7 ADF10087	7 ADF09982	7 ADJ80262	8 ADO07331	9 ADY75436	9 AEB13589	9 AEB13642	9 AED04308	9 AED06937	10 AEE47598	10 AEF18501	4 AAE06948	4 AAE06996	4 AAU09920	7 ABR61476	8 ADQ89233	8 ADQ89281
	Query Match Length DB	260	110	93	100	100				100		100			100		100	100	111	111			111	111
di	Query Match	75.9	19.5	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4
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9 ADU26553 9 AEB09554 9 AEB09506	9 AEC92164 2 AAW79227 2 AAW53585 4 AAE07003	4 AAE06993 4 AAE06999 5 ADF98232	8 ADQ89284 8 ADQ89278 8 ADQ89288	9 AEB09557 9 AEB09551 9 AEB09561	8 ADO07283 9 ADZ42043 9 ADZ42042 9 ADZ42041 10 AEG01367
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ALIGNMENTS

cytostatic; immunostimulant; pharmaceutical; protein interaction; therapeutic; immune modulation; solid tumor; leukemia; colorectal tumor; breast tumor; uterine cervix tumor; uterine fibroids; ovary tumor; gynecology and obstetrics; polycystic ovary syndrome; antiinfertility; gynecology; genitourinary disease; prostate tumor; prostate disease; andrology; genitourinary disease; pituitary tumor; endocrine disease; andrology; melanoma; bone tumor; musculoskeletal disease; multiple myeloma; melanoma; heatological disease; immune disorder; central nervous system tumor; neurological disease; glioma; astroblastoma; neoplasm; single chain antibody; BC-12. Single chain variable fragment antibody BC-12 protein SEQ ID NO 2. AEC92007 standard; protein; 260 AA. (first entry) Homo sapiens. 01-DEC-2005 AEC92007; AEC92007

Synthetic.

/note= "Encoded by ATG" /note= "Encoded by GCA" Location/Qualifiers Misc-difference 1. Misc-difference 62

WO2005091805-A2

14-FEB-2005; 2005WO-US004612.

13-FEB-2004; 2004US-0544807P. 10-NOV-2004; 2004US-0626726P. 11-FEB-2005; 2005US-00056825.

Saven A; Janda KD, (SCRI) SCRIPPS RES INST. Felding-Habermann B,

WPI; 2005-664872/68. N-PSDB; AEC92006.

Humanized antibody, antibody engineering; fab; cytomegalovirus infection.

HCMV-Fab-6 amino acid sequence #1.

Human herpesvirus

CN1445243-A.

01-OCT-2003

Fab antibody of human resourced neutrality genetic engineering for anti

Disclosure; Fig 3b; 15pp; Chinese.

human cytomegalo virus.

DI.

(VIRU-) INST VIRUS PREVENTION & CONTROL CHINA

Duan T;

Gu S,

Liang M,

WPI; 2004-091790/10.

N-PSDB; ADW24448

13-DEC-2002; 2002CN-00155426 13-DEC-2002; 2002CN-00155426

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Specifically produced on a cell in a metastatic state compared to a similar, non-metastatic cell, and does not bind to a non-activated alphavbeta 3 integrin receptor. Also described are: a pharmaceutical composition comprising the antibody; treating a disease state in a mammal; a cell line comprising the antibody; treating a disease state; homing propensity to a target tissue; producing an antibody phage population having affinity for a tumor cell target; detecting tumor cells in a mammal by treatment with a cancer therapeutic; inducing or enhancing an immune response to an antigen in a mammal; detecting una cells in a mammal by treatment with cancer therapeutic; inducing or enhancing an immune response to an antigen in a mammal; detecting una cervated cell surface in a mammalian tissue sample; interfering with cells liable to undergo metastasis associated with a disease state; dentifying cells liable to undergo metastasis cassociated with a disease state; an isolated 80-12 or 80-15 polymucleotide comprising a nucleotide sequence that has at least 90% sequence that has at least 90% sequence that has at least 90% sequence that has at least 90% sequence that has at least 90% sequence identity to SEQ ID NO.

1 or 3 given in the specification; an isolated bolypeptide comprising a nucleotide sequence that has at least 90% sequence that has at least 90% sequence of the polymucleotide in which the nucleotide sequence of the polymucleotide in which the nucleotide sequence of the polymucleotide in which the nucleotide sequence of the polymucleotide in a host cell; a host cell comprising the polymucleotide or progeny of the cell; and determining anti-metastatic comprising cancer, leavening neoplastic disease, solid tumor, hematological malignancy, reating neoplastic disease, solid tumor, hematological malignancy, reating neoplastic disease, solid tumor, hematological malignancy uterine leidence that has noner, anterine concertal cancer, benign or malignant preast cancer, uterine concertal cancer, anterine concertal cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
  .c. o.rv bc-12 or Bc-15 antibody comprises ligand mimetic, which specifically binds to activated alphavbeta3 integrin receptor, useful for treating, e.g. neoplastic disease, solid tumor, leukemia, or benign or malignant breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKFQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSSGGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSGGGGSGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSGGGGSGGCGSEIVITQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQGT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 QKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSSGGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer, uterine leiomyomas, ovarian cancer, endometrial cancer, polycystic ovary syndrome, endometrial polyps, prostate cancer, prostatic hypertrophy, pituitary cancer, adenomyosis, adenocarcinomas, meningioma, melanoma, bone cancer, multiple myeloma, CNS cancer, glioma, or astroblastoma. This is the amino acid sequence of single chain variable fragment antibody BC-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                     The invention describes an antibody comprising a ligand mimetic, w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 198; DB 9; Length 260;
Pred. No. 3.8e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.9%; Scc...
100.0%; Pred. No....
0; Mismatches
                                                                                                                                                                Claim 2; SEQ ID NO 2; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVEIKRGLGGLVDYKDDD 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                          The invention relates to a humanized neutral genetically engineering Fab fragment, gene product and application are also disclosed. The Fab recombinant antibody is determined by the specific gene sequence in the hypervariable region of the light-chain and heavy-chain variable regions. The antibody can be used for preventing and treating the diseases associated with HCMV infection. The current sequence represents a HCMV-Fab-6 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoproliferative disorder; vaccine; gene therapy; immunoglobulin; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 YLSWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunoglobulin kappa light chain protein 5.
                                                                                                                                                                                                                                                                                                                                                                                                                19.5%; Score 51; DB 8; Le
100.0%; Pred. No. 2.6e-34;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CABL-) CANADIAN BLOOD SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADU04216 standard; protein; 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-APR-2004; 2004WO-CA000544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-2003; 2003US-0461137P. 30-SEP-2003; 2003US-0506779P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virucide:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viral infection;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004090544-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADU04216;
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ADW24449 standard; protein; 110 AA.

ADW24449 RESULT

(first entry)

10-MAR-2005 ADW24449;

XXXE,

KVEIKRGLGGLVDYKDDD 260

Hu Y,

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The invention relates to the use of human anti-cytotoxic T lymphocyte antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer, testicular cancer, uterine cancer and carcinoma of the fallopian tubes. The present sequence is human A10/A26 antibody light chain germline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
                                                                                                                                                                                                              Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the preparation of medicament for the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a method of making a humanised antibody, comprising making chimeric antibodies containing a complementarity determining region (CDR) from a non-human antibody and appropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 WFQORPGOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human germline light chain variable region gene segment #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, light chain variable region, VK, humanised antibody, chimeric antibody, complementarity determining region, CDR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%; Score 48; DB 6; L
100.0%; Pred. No. 7.5e-32;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein. This sequence is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO27142 standard; protein; 100 AA
                                                                                                                                                                                                                                                                                      Disclosure, Fig 7; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 2; 31pp; English.
                        23-MAY-2001; 2001US-0293042P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   canonical CDR structure type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-2002; 2002US-00194975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUL-2001; 2001US-0305111P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 48; Conservative
                                                                   (PFIZ ) PFIZER PROD INC
                                                                                                                  Mueller EE;
                                                                                                                                                                 WPI; 2003-131215/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-492151/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003039649-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FOOT/) FOOTE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                    Hanson DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO27142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poote J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB027142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for characterising a viral infection in a host. The method comprises identifying at least one viral based sequence element in a blological sample obtained from the host, determining a homology profile of the viral-based sequence element with at least one endogenous host element and characterising the viral infection based on the homology profile, where the homology profile is indicative of a viral behaviour of the viral infection in the host. The method of the invention demonstrates virucide applications and may be useful for preparing a medicament for detecting and/or treating a viral infection or related condition, such as an autoimmune disease e.g. type is cryoglobulinaemia, or lymphoproliferative disease. The viral infection may be due to HCV (Hepatitis C virus), HIV or a member of a infection may be due to HCV (Hepatitis C virus), HIV or a member of a cornaviridae, plaviviridae, papillomaviridae or Coronaviridae, plaviviridae, papillomaviridae or Coronaviridae virus family. Treatment of the invention may be useful for detecting the presence of a virus in a biological sample or for manufacturing a medicament for treating SARS coronavirus (SARS-COV) and/or Human T-lymphotropic virus (HTV-I) infection. The methods are further useful for developing treatment requests to target genotype-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                             Characterizing a viral infection in a host, for developing treatment for severe acute respiratory syndrome-coronavirus (SARS-CoV), by determining homology profile of a viral-based sequence element with an endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CDR) 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complementarity determining region (CDR) 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specific viral variants. The current sequence is that of a human immunoglobulin light chain kappa (IgVLk) protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 8; Le
Pred. No. 7.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human A17 antibody light chain germline protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%; Sco. No. 100.0%; Pred. No. . . . . . Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE35907 standard; protein; 100 AA
                                                                                                                                                                                                                                       Example 1; Fig 24; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2002; 2002EP-00253652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C
94. .100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24. .39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                   WPI; 2004-766498/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                   Brown E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1262193-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Best Loca Matches

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RESULT 4 AAE35907 Region Region Region

; 0

Gaps

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0; Indels

Length 100;

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humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparing tramework sequences between non-human and human antibodies. This sequence represents a human light chain variable region gene segment used in the creation of humanised antibodies
framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibodies as the basis for selection, for humanisation. The method is useful for making a humanised antibody or a converted antibody. The method is applicable for converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable human framework sequences to support non-human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for direct comparison of framework sequences, without the need for determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain
          05555555555555555555555555838
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Sequence 100 AA;

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                                  Gaps
                                ö
                                                       WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220
                                                                  WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
           Length 100;
                                0; Indels
        Score 48; DB 6; Lo
Pred. No. 7.5e-32;
                                Mismatches
18.4%; Scc.
100.0%; Prev
                                Conservative
                   Local Similarity
                                48;
                                                       173
                                                                            40
           Query Match
                      Best Loc
Matches
                                                        ð
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ADF10189 standard; protein; 100 AA ADF10189 RESULT

ADF10189;

(first entry) 12-FEB-2004

Antibody light chain variable region VLk_2-30.

Antibody; stability; solubility; antigen binding affinity; variable region; human

Homo sapiens

WO2003074679-A2

12-SEP-2003.

03-MAR-2003; 2003WO-US006598.

01-MAR-2002; 2002US-0360843P. 29-MAY-2002; 2002US-0384197P.

(XENC-) XENCOR

Marshall SA, Desjarlais JR, Lazar GA,

WPI; 2003-722066/68

Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable positions.

Example 16; Fig 40b; 135pp; English

The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the

DB 7; Length 100;

18.4%; Score 48;

Query Match

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antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody variable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                       173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
                                                                                                                                                                                                       Length 100;
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                                                                                                                                                                                                       18.4%; Score 48; DB 7; Length 100
100.0%; Pred. No. 7.5e-32;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGF antibody light chain variable region VLk_2-30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marshall SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Fig 16b; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF10087 standard; protein; 100 AA.
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29-MAY-2002; 2002US-0384197P.
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Best Local Similarity 100.0
Matches 48; Conservative
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                                                                                                                                                                   Sequence 100 AA;
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hybrid antibody; antibody; framework region; homology; immunogenicity.

03-DEC-2002; 2002WO-US038450. 03-DEC-2001; 2001US-0336591P.

WO2003048321-A2 Homo sapiens

12-JUN-2003

(ALEX-) ALEXION PHARM INC

WPI; 2003-513753/48.

Rother R,

Vkappa gene locus antibody amino acid sequence #22.

06-MAY-2004 (first entry)

ADJ80262;

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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical property of antibody, especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody way be variable region sequence used to illustrate the invention.
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                      Gaps
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                                                                                                                                                                                                                                                                                                             Antibody; stability; solubility; antigen binding affinity; variable region; human.
                                                                           40 WFQQRPGQSPRRLIXKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED
                                                        173 WFOORPGOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED
                      Indels
Pred. No. 7.5e-32;
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                                                                                                                                                                                                                                                                             Antibody light chain variable region VLk 2-30.
   Best Local Similarity 100.0%; Pred. No. 7.5
Matches 48; Conservative 0; Mismatches
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                                                                                                                                                                         ADF09982 standard; protein; 100 AA.
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29-MAY-2002; 2002US-0384197P.
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                                                                                                                                          RESULT 8
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Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.

Disclosure; SEQ ID NO 22; 77pp; English.

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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (i) providing an initial antibody having expecificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database of than the first component, the second component selected from the group selecting a second component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vi) comparing the sequence of the second component to sequences contained in a reference database of the second component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (viii) selecting a sequence from the database of antibody than the selected antibody; and (ix) operatively linking the sequences of the initial antibody; and (ix) operatively linking the antibody fragment. The method is useful for producing a hybrid antibody fragment. The method is useful for producing a hybrid antibody or hybrid antibody tragment (claimed). The antibody variable heavy or hybrid antibody fragment can expend the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while mathod and sequence of an antibody from the Vkappa gene locus.
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Best Local Similarity
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Gaps

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0; Indels

Score 48; DB 7; Length 100; Pred. No. 7.5e-32;

48; Conservative

Matches

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Query Match Best Local Similarity

Sequence 100 AA;

87

173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220

40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED

ADJ80262 standard; protein; 100 AA

ADJ80262 ID ADJ8

RESULT 9

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WO2004033658-A2
                     Homo sapiens
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recombinant catalytic polypeptides of the invention. These comprise a human antibody light chain operably joined to a heterologous antibody human antibody light chain has a serine protease dyad and endopeptidase activity, and the heavy chain has a predetermined specificity for a target protein. By joining 2 heterologous human antibody chains, one of which supplies the catalytic activity to hydrolyse polypeptides and the chart the binding specificity for a target protein, the invention provides for the construction of a repertoire of proteases with customised protein substrate specificities of potentially unlimited number and thus makes possible the effective treatment and/or prevention of any medical condition attributable to the presence or overexpression of any medical condition attributable to the presence or overexpression of any dentified protein. The invention also provides nucleic acids cnocding the catalytic antibodies (which can be used for gene therapy), host cells, transgenic non-human animals, and methods of cleaving a recombinant catalytic polypeptides with altered enzymatic activity, and a method of altering the enzymatic activity, and a method of altering the enzymatic activity, and a method of altering the enzymatic activity of the recombinant catalytic contents.
A17. This is one of a repertoire of human kappa light chain sequences ADO07310-ADO07349 screened for putative catalytic triads. Several genes encoding such light chains ADO07282-ADO07309 were cloned for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutating at least one complementarity determining region of the heavy chain. A serine protease triad was identified in the present sequence, which can be used as the light chain sequence in catalytic polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 18.4%; Score 48; DB 8; Le
Local Similarity 100.0%; Pred. No. 7.5e-32;
hes 48; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant catalytic polypeptide useful for cleaving target proteins or for treating or preventing cancers, comprises a human antibody light chain operably joined to a heterologous antibody heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Possible Ser component of catalytic triad"
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/note= "Complementarity determining region 3"
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                                                                                                                                                                 Catalytic antibody; human; antibody; gene therapy; protease.
                                                                                                                   Human antibody A17 light chain variable region.
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Label= CDR1
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||abel= FR1
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Gaps

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Length 100;

87

Producing polynucleotide encoding human germline antibody V-region for generating full-length antibody germline V-region genes, by obtaining N or J minigene and joining V minigene with J minigene, or joining J minigene with V minigene. Disclosure; Fig 12; 52pp; English.

The present sequence is the light chain variable region of human antibody

Disclosure, Fig 3, 92pp, English.

The present invention relates to producing germline antibody genes by a completely in vitro approach that mimics the natural process of V(D)J crecombination. The antibody genes are completely human and native in the recomplation that with an expension of their sequence, and libraries of such antibody genes can be constructed which represent an unselected population representing the entire antibody crepertoire. The method uses gene amplification to produce a V minigene, and a hybrid primer fapable of hybridizing to a V minigene and either a D or V minigene. The hybrid primer facilitates recombination of a V contingene to a D or J minigene to produce a full length V-region gene. Also disclosed is a library comprising member polymucleotides encoding exogenously rearranged human germline antibody V-region, a D minigene or solution to the 3 minigene in so betained by chemical contingene. The V minigene or the J minigene in so betained by chemical synthesis or by amplification from a germline DNA library. Joining the V minigene with at least two or three oligonucleotide primers. The V minigene is derived from human immunoglobulin heavy chain locus. The V-region also comprises a serine protease triad. The human immunoglobulin heavy chain locus. The V-region also be used as precursors to more high affinity antibodies, and are useful in the generation of efficiently pairing libraries of heavy and light chains. The present sequence is a human germline light chain kappa region peptide

Sequence 100 AA;

Gaps ö 173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220 87 Length 100; 40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 18.4%; Score 48; DB 9; Length 100 100.0%; Pred. No. 7.5e-32; ive 0; Mismatches 0; Indels Conservative Local Similarity 48; Query Match Matches 8 g

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AEB13589 standard; protein; 100 AA. AEB13589; RESULT 12 AEB13589

(first entry) 25-AUG-2005 Human variable heavy chain region protein, VH_3-43.

protein engineering; immunogenicity; germ cell; heavy chain variable region; antibody.

Homo sapiens.

WO2005056759-A2

23-JUN-2005.

04-DEC-2003; 2003US-0527167P. 21-JUN-2004; 2004US-0581613P. 13-AUG-2004; 2004US-0601665P. 16-OCT-2004; 2004US-0619483P.

03-DEC-2004; 2004WO-US040694

(XENC-) XENCOR INC

Hammond PW; Lazar GA, Desjarlais JR,

WPI; 2005-458579/46.

Generating variant protein for host, by comparing parent protein sequence with natural protein sequences from host, analyzing and substituting amino acids of parent sequences with corresponding amino acid string of natural sequence

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                                                               for a host. The method involves comparing a parent protein sequence with natural protein sequences from a host, analyzing the amino acid strings of the parent sequences with corresponding amino acid strings of each of protein sequences with corresponding amino acids of parent protein sequences with corresponding amino acids of a natural protein sequences on an amino acid string. The method is useful for generating a variant protein. The method enables the generation of variant protein. The method enables the generation of variant proteins having an increased host string content and reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for generating a variant protein for a host. The method involves comparing a parent protein sequence with natural protein sequences from a host, analyzing the amino acid strings of the parent sequence with corresponding amino acid strings of each of the natural protein sequences, and substituting amino acids of parent protein sequences with corresponding amino acids of parent
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                            immunogenicity. This sequence represents a variable heavy chain of a
human antibody protein used in a human germ line comparison of the
                                                invention relates to a novel method for generating a variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein engineering; immunogenicity; germ cell; light chain variable region; antibody.
                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. 7.5 ive 0; Mismatches
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                   Disclosure; Fig la; 137pp; English.
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21-JUN-2004; 2004US-0581613P.
13-AUG-2004; 2004US-0601665P.
16-OCT-2004; 2004US-0619483P.
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                                                                                                                                                                                                                                                                                                                                                                                               48; Conservative
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                                                                                                                                                                                                                                                                                                                       Sequence 100 AA;
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protein sequence on an amino acid string. The method is useful for generating a variant protein, e.g. a variant antibody for a host as compared to a parent protein. The method enables the generation of variant proteins having an intended host string content and reduced immunogenicity. This sequence represents a variable light chain of human antibody protein used in a human germ line comparison of the
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Sequence 100 AA;

Gaps ö 18.4%; Score 48; DB 9; Length 100; 100.0%; Pred. No. 7.5e-32; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 48; Conservative ઠ

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AED04308 standard; protein; 100 AA (first entry) 01-DEC-2005 AED04308; RESULT 14 AED04308

Human anti-CTLA-4 antibody, Kappa chain protein SEQ ID NO:36.

cancer; cytostatic; neoplasm; antibody; antibody therapy; igg; CTLA-4; cytotoxic T lymphocyte antigen-4.

Homo sapiens

WO2005092380-A2

06-OCT-2005

14-MAR-2005; 2005WO-IB000671.

26-MAR-2004; 2004US-0556801P.

(PFIZ) PFIZER PROD INC.

DA; Noe Mueller EE, Gomez-Navarro J, Hanson DC,

WPI; 2005-684091/70.

Treating cancer in mammal who has undergone stem cell transplantation, comprises administering human anti-cytotoxic T lymphocyte antigen-4 antibody to the mammal.

Disclosure; SEQ ID NO 36; 135pp; English.

The invention relates to a method of treating (M1) cancer in a mammal comprising administration of a human anti-CTLA-4 (cytotoxic T lymphocyte antigen-4) antibody. Also included are: treating cancer in a mammal by administering cancer in a mammal by administering anti-CTLA-4 antibody; and treating cancer in a mammal by administering an effective amount of a human anti-CTLA-4 antibody; and transplantation. The cancer is chosen from breast cancer including metastatic breast cancer, is chosen from breast cancer including cancer, pancreatic cancer, skin cancer, cancer of the head or neck, melanoma including coetaneous or interlobular malignant melanoma, uterine cancer, covarian cancer, resticular cancer, uterine cancer, cancer defined cancer, testicular cancer, uterine cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined cancer, cancer defined c intestine, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethyroid gland, cancer of the penis, prostate cancer, chronic acute leukemias including acute myeloid leukemia, chronic myeloid

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leukemia, acute lymphoblastic leukemia, chronic lymphocytic leukemia, solid tumors of childhood, lymphocytic lymphomas, cutaneous T cell lymphoma, cancer of the bladder, cancer of the kidney or ureter, renal cell carcinoma, carcinoma of the ranal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor anglogenesis, spinal axis tumor, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally induced cancers including those induced by asbestos, myeloma, neuroblastoma, and pediatric sarcomas. The present sequence represents human anti-CTLA-4 antibody, Kappa chain protein SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selecting an antibody with a reduced risk of inducing a human anti-human antibody response comprises providing an immunoglobulin gene encoding a candidate antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody therapy; antibody engineering; transgenic animal; drug screening; leukemia; hematological disease; neoplasm; cytostatic; autoimmune disease; immunosuppressive; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                               40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED
                                                                                                                                                                                                                                                                           Length 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human antibody Vkappa protein sequence, SEQ ID NO:107.
                                                                                                                                                                                                                                                                         18.4%; Score 48; DB 9; Lv
100.0%; Pred. No. 7.5e-32;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AED06937 standard; protein; 100 AA
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24-MAY-2004; 2004US-0574661P.
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                                                                                                                                                                                                                                                                                                                    48; Conservative
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                                                                                                                                                                                                                                                                                               Local Similarity
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is a V gene, e.g. a VH (heavy) gene or a VL (light) gene. The methods are useful for selecting an antibody with a reduced risk of inducing HAHA response. The antibody, composition, and method are useful for treating diseases, e.g. leukemia or autoimmune diseases. The present sequence is a human antibody Vkappa protein sequence.
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Sequence 100 AA;

ö Gaps .; 0 Query Match
18.4%; Score 48; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.5e-32;
Matches 48; Conservative 0; Mismatches 0; Indels

ò q Search completed: August 9, 2006, 13:34:15 Job time : 196 secs

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RESULT 2
US-10-194-975-75
Squence 75, Application US/10194975
Patent No. 6881557
GENERAL INFORMATION:
APPLICANT: FOOTE, Jefferson
TITLE NOT INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT PILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
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                                                                                                                                         9, 2006, 13:39:38 ; Search time 49 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-477-2818-89

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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                          Sequence:
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67, Appl
61, Appl
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58, Appl
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MELLER, EILLEN E.
APPLICANT: MUSICIER, EILLEN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCIONAL ANTIBODIES TO CTLA-4
FILE REPERENCE: ABS.-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR PILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 100;
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100.0%; Pred. No. 7.8e-30;
tive 0; Mismatches 0;
US-09-840-459-69
US-08-45-89A-105
US-08-545-89A-105
US-09-515-697-105
US-09-818-247-22
US-09-840-459-67
US-09-497-625A-67
US-09-497-625A-61
US-09-497-625A-63
US-09-497-625A-63
US-09-497-625A-63
US-09-459-63
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US-09-459-63
US-09-450-63
US-09-450-63
US-09-840-459-63
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US-09-840-459-63
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; Sequence 113, Application US/09472087
; Patent No. 6682736
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 113
LENGTH: 100
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US-09-472-087-113
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US-09-497-625A-11
           LENGTH: 111
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Patent No. 669650

GENERAL INFORMATION:
APPLICANT: LARGAS, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Erien, Siobhan H.
APPLICANT: O'Erien, Siobhan H.
APPLICANT: O'Erien, Siobhan H.
APPLICANT: O'Erien, Siobhan H.
APPLICANT: O'Erien, Siobhan H.
APPLICANT: O'Erien, Siobhan H.
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REPERBRECE: 1855.1052-012
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR PELICATION NUMBER: 09/497,625
PRIOR PELICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR PILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAUES FRAU
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Patent No. 6663863
GENERAL INFORMATION:
APPLICANT: HOWATH, Christopher J.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Neetenosis
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR PLICATION NUMBER: US 09/528,267
PRIOR PLING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PRASESO for Windows Version 4.0
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Pred. No. 7.8e-30;
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 48; Conservative
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Best Local Similarity 100.
Matches 48; Conservative
; SEQ ID NO 75
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-75
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-739-13
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                                                                                   18.4%; Score 48; DB 2; Length 111; 100.0%; Pred. No. 8.4e-30; Live 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 8.4e-30;
Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-840-459-59
; Sequence 59, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LARGAR, Gregory J.
; APPLICANT: Newman, Walter
; APPLICANT: Newman, Walter
; APPLICANT: Ones, S. Tarran
; APPLICANT: O'Reefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: HUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2001-02-03
; PRIOR FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR PLILING DATE: 1999-07-22
; PRIOR FILING DATE: 1999-07-23
; PRIOR FILING DATE: 1998-07-23
; PRIOR FILING DATE: 1998-07-23
; PRIOR FILING DATE: 1998-07-23
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Sequence 11, Application US/09497625A

Patent No. 6727349

GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Howman, Walter
APPLICANT: Owner, S. Tarran
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-004
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 111
                                                                                                                                              48; Conservative
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US-09-840-459-59
; ORGANISM: Homo sapiens
US-09-840-459-11
                                                                                                                   Best Local Similarity
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US-08-477-877B-89
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                                                                                                                                                                                                                                                                                                                0; Indels
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APPLICANT: LaRosa, Gregory J.
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: O'Serien, Siobhan H.
APPLICANT: O'Serien, Siobhan H.
APPLICANT: O'Serien, Siobhan H.
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
FILLE REPERERENCE: 1855.1052-004
FILLE REPERERENCE: 1855.1052-004
CURRENT APPLICATION NUMBER: 09/359,193
PRIOR PELICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/321,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SEQ ID NO 59
LENGTHALE.
LENGTH: 111
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Anthony R.
Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
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2100 Pensylvania Avenue, N.W.
                                                                                                                                                                                                                                                           Query Match 18.4%; Score 48; DB 2; I Best Local Similarity 100.0%; Pred. No. 8.4e-30; Matches 48; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 111
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Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: REES, Anthony R.
APPLICANT: REES, Anthony R.
APPLICANT: GUILD,
TITLE OF INVENTION: SURFACE RESIDUR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/09497625A Patent No. 6727349
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ADDRESSEE: Sughrue, N
STREET: 2100 Pensylva
                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-497-625A-59
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Sequence 89, Application US/08477877B

Patent No. 5730979

GENERAL INFORMATION:
APPLICANT: Latinne, Dominique
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANT: Latinne, Dominique
TITLE OF INVENTION:
ADDRESSER: Carella, Byrne, Bain, Gilfillan,
ADDRESSER: Carella, Stewart & Olstein
STREET: Reseland
STREET: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: Wordderfect 5.1
COMPUTER: Wordderfect 5.1
CURRENT APPLICATION NUMBER: US/08/477,877B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.4%; Score 48; DB 1; Length 112; Best Local Similarity 100.0%; Pred. No. 8.5e-30; Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,877B
FILING DATE: 07-JUN-1995
CLASSIFFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: 01stein, Ellict M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 24,025
REPERENCE/DOCKET NUMBER: 21,025
TELECHONE: 201-994-1700
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7860
TELERAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-07-942-245-28
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Gaps
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                                             173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220
                                                                      40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
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    0; Indels
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                                                                                                                                                                                                                                                                                                                          APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Rieber-Emmons, Thomas
APPLICANT: White-Schaff, Mary
TITE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Light chain vairable region of NAME/KEY: HUM5400
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.4%; Score 48; DB 100.0%; Pred. No. 8.5 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61750-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
                                                                                                                                                                          US-08-477-989B-89; Sequence 89, Application US/08477989B; Patent No. 5951983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Cecchi, Stewart E
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
APPLICANT: Kaplan, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 89:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 112 amino acids amino acids
    48; Conservative
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Best Local Similarity
Matches 48; Conserv
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  Matches
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APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
NUMBER OF SEQUENCE: 96
CORRESPONDENCE ADDRESS:
ADDRESSE: Carella, Byrne, Bain, Gilfillan,
ADDRESSE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
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                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                               173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220
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                                                                                                                                                                                                                                      Score 48; DB 1; Length 112;
Pred. No. 8.5e-30;
0; Mismatches 0; Indels
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Pred. No. 8.5e-30;
                                                                                                                                               FEATURE:

NAME/KEY: Light chain vairable region of HUM5400
US-08-477-877B-89
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US-08-472-281A-89
                                                                                                                                                                                                                                        Query Match
18.4%; Score 48; DB :
Best Local Similarity 100.0%; Pred. No. 8.5s
Matches 48; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 89, Application US/08472281A Patent No. 5817311
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.4%; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
                                         LENGTH: 112 amino acida
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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TELEFAX: 2
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RESULT 15
US-09-497-625A-56
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US-09-840-459-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED
                                                                                                                                 GENERAL INCORPATION:
APPLICANT: LaROSA, Gregory J.
APPLICANT: LaROSA, Gregory J.
APPLICANT: Horvarin, Christopher
APPLICANT: Horvarin, Christopher
APPLICANT: Ones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, BETHERES
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2001-02-03
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOUTWARE FASTESE FASTESE FOUNDER: 107
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Norman, Walter
APPLICANT: O'Reien, Siobhan H.
APPLICANT: O'Reien, Siobhan H.
APPLICANT: O'Reien, Siobhan H.
APPLICANT: O'Reien, BETHORS DANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HOWBER: US/09/840,459
FILLE REFERENCE: 1855.1052-012
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 107
SOUTWARE: FESTESEQ for Windows Version 3.0
                                                                                         Sequence 56, Application US/09840459
Patent No. 6696550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-840-459-62
; Sequence 62, Application US/09840459
; Patent No. 6696550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                     JS-09-840-459-56
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LENGTH: 112
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LENGTH: 112
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                                                                                                             173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220
                                                                                                                                        40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
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Query Match 18.4%; Score 48; DB 2; Length 112; Best Local Similarity 100.0%; Pred. No. 8.5e-30; Matches 48; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                              GARMEAL INTORNATION:

APPLICANT: LARGEA, Gregory J.

APPLICANT: Newman, Walter

APPLICANT: Newman, Walter

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Brien, Siobhan H.

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

TITLE OF INVENTION: METHODS OF USE THEREFOR

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REPERENCE: 1855.1052-012

CURRENT FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-03

PRIOR FILING DATE: 1999-07-22

PRIOR FILING DATE: 1999-07-22

PRIOR FILING DATE: 1999-07-23

PRIOR FILING DATE: 1999-07-23

PRIOR FILING DATE: 1999-07-23

PRIOR FILING DATE: 1999-07-23

NUMBER OF SEQ IO NOS: 107

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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GENERAL INCOMATION:
GENERAL INCOMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Horvath, Christopher
APPLICANT: Oones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-004
CURRENT TILING DATE: 1855.1052-004
CURRENT FILING DATE: 1999-07-223
PRIOR FILING DATE: 1999-07-223
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 2; Lo
Pred. No. 8.5e-30;
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Patent No. 6727349
                                                                                                                                                                                                                                                                                               Sequence 66, Application US/09840459
Patent No. 6696550
GENERAL INFORMATION:
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US-09-840-459-66
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Best Local Similarity
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Query Match 18.4%; Score 48; DB 2; Length 112; Best Local Similarity 100.0%; Pred. No. 8.5e-30; Matches 48; Conservative 0; Mismatches 0; Indels
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Search completed: August 9, 2006, 13:41:02 Job time : 50 secs

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LENGTH: 261
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:: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-153-382-36
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US-10-153-382-87
US-10-10-153-89-82
US-10-10-153-89-82
US-11-084-554-107
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US-11-084-659-111
US-10-66-773-111
US-10-766-610-111
US-10-766-610-111
US-10-766-610-111
US-10-73-563-111
US-10-73-563-111
US-10-73-563-11
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                           2097797 seqs, 463214858 residues
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                                   OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Sequence 2, Application US/11056825

Sequence 2, Application US/11056825

Fublication No. US20050255109A1

GENERAL INFORMATION:

APPLICANT: Belding-Habermann, Brunhilde

APPLICANT: Janda, Kim D.

APPLICANT: Belding-Habermann, Brunhilde

APPLICANT: Saven, Alan

TITLE OF INVESTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS

FILE REPERENCE: SCRP-0042

CURRENT PAPLICATION NUMBER: US/11/056,825

CURRENT PILING DATE: 2005-02-11

PRIOR FILING DATE: 2004-11-10

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.3
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100.0%; Pred. No. 7.4e-201;
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US-09-840-459-56
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US-09-840-459-66
US-10-766-773-62
US-10-766-773-66
US-10-766-610-56
US-10-766-610-66
US-10-766-610-66
US-10-733-563-66
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US-10-733-748-1964
US-10-293-418-1964
US-11-054-515-1964
US-10-293-444-1964
US-10-766-773-60
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Best Local Similarity 100.
Matches 261; Conservative
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40 WFQQRPGQSPRALIYKVSNRDSGVPDRFSGSGSGGTDFTLKISRVEAED 87
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Best Local Similarity
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; ORGANISM: human
US-10-308-817-22
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LENGTH: 100
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                                                                                                                                                  APPLICANT: Janda, Kim D.
APPLICANT: Saven, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REPERENCE: SCRP-004.
CURRENT APPLICATION NUMBER: US/11/056,825
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR PILING DATE: 2004-11-10
PRIOR PILING DATE: 2004-11-10
PRIOR PILING DATE: 2004-11-10
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Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Poote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: S01231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENGTH: 100
                                                              Sequence 7, Application US/11056825
Publication No. US20050255109A1
GENERAL INFORMATION:
APPLICANT: Felding-Habermann, Brunhilde
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SOFTWARE: Patentin version 3.3
SEQ ID NO 7
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Matches 48; Conservative
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ORGANISM: Homo sapiens
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US-10-194-975-75
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                  RESULT 2
US-11-056-825-7
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18.4%; Score 48; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 48; Conservative 0; Mismatches 0; Indels
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RESULT 4
US-10-153-382-36
US-10-153-382-36
Sequence 36, Application US/10153382
Sequence 36, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT FILIG DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 6/293042
PRIOR APPLICATION NUMBER: 6/293042
PRIOR PILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
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Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERRNCE: 1087-37
CURRENT FILING DATE: 2002-12-03
CURRENT FILING DATE: 2005-12-03
WUNDER OF SEC ID NOS: 195
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
WUMBER OF SEQ ID NOS: 196
SOPTWARE: Patentin version 3.2
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; Sequence 22, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
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173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220

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Query Match
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APPLICANT: Mark J. Neveu
APPLICANT: Blien B. Mueller
APPLICANT: Steven C. Gilman
APPLICANT: Steven C. Gilman
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: DOSE R. COTVALAN
FILE REFERENCE: ABX-PF1 DIV1
CURRENT APPLICATION NUMBER: US/09/472087
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFFWARE: PatentIn Ver. 2.1
                                                                                                                                      Length 100;
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18.4%; Score 48; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 48; Conservative 0; Mismatches 0; Indels
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                                                                                                                                    Score 48; DB 4; Le Pred. No. 1.4e-30;
                                                                                                                        18.4%; Scc...
100.0%; Pred. No. 1...
'... 0; Mismatches
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Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Dahiyat, Bassil I.
TILE OF INVENTION: ANTIBODY OFTMIZATION
FILE REPERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR PILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2005-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
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Publication No. US20040228858A1
GENERAL INFORMATION:
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                                                                                                                                      Query Match
Best Local Similarity
Matches 48; Conserva
; SEQ ID NO 22
; LENGTH: 100
; TYPE: PRT
; ORGANISM: human
US-10-453-698-22
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LENGTH: 100
TYPE: PRT
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APPLICANT: Eileen E. Mueller
APPLICANT: Steven C. Gilman
APPLICANT: Steven C. Gilman
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
CURRENT BILLING DATE: 2004-02-10
PRIOR FILING DATE: 2003-07-01
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113647
PRIOR PILING DATE: 1998-12-23
PRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 113
LENGTH: 100
                                                                                    Length 100;
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APPLICANT: Hanson, Douglas C.
APPLICANT: Hanson, Douglas C.
APPLICANT: Bileen, Muchler Elliott
APPLICANT: Noe, Dennis A.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC32177A
CURRENT PELICATION NUMBER: US/11/085,368
CURRENT FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: US 60/556,801
PRIOR APPLICATION NUMBER: US 60/556,801
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN VETSION 3.3
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                                                                              18.4%; Score 48; DB 5; L
100.0%; Pred. No. 1.4e-30;
tive 0; Mismatches 0;
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18.4%; Score 48; DB
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 48; Conservative 0; Mismatches
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Publication No. US20050226875A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
                                                                                                                                                                                                                                                                                                                                                                                                     US20040228861A1
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                                                                                                                                     48; Conservative
; ORGANISM: Homo sapiens
US-10-612-497-113
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US-10-776-649-113
                                                                                                    Best Local Similarity
Matches 48; Conserv
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US-10-776-649-113
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LENGTH: 100
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APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
TITLE OF INVENTION: REDUCING THE RISK OF HUWAN ANTI-HUWAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE REFERENCE: ABGRNIX.100A
CURRENT FILING DATE: 2005-03-17
PRIOR FILING DATE: 2005-03-17
PRIOR FILING DATE: 2005-03-19
PRIOR APPLICATION NUMBER: 60/554,561
PRIOR FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 266
SOFTWARE: PASKSEQ for Windows Version 4.0
LENGTH: 100
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                                                                          Ouery Match 18.4%; Score 48; DB 6; Length 100; Best Local Similarity 100.0%; Pred. No. 1.4e-30; Matches 48; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.4e-30;
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TILLE REPERENCE: 30219/UG/S
FILE REPERENCE: 30219/UG/S
FULE REPERENCE: 30219/UG/S
CURRENT APPLICATION NUMBER: US/11/054,669
FURE APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PetentIn version 3.3
SEQ ID NO 75
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Publication No. US20050260679A1
GENERAL INFORMATION:
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; Sequence 75, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-085-368-36
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APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, John R.
APPLICANT: Desjarlais, John R.
APPLICANT: Bemond, Phillip W.
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION NUMBER: US 60/527,167
PRIOR FILING DATE: 2003-12-04
PRIOR PLICATION NUMBER: US 60/51,65
PRIOR PLICATION NUMBER: US 60/601,665
PRIOR APPLICATION NUMBER: US 60/619,483
PRIOR PLING DATE: 2004-08-13
PRIOR PLING DATE: 2004-09-14
PRIOR PLING DATE: 2004-010-14
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PATENTIN Version 3.3
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40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
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Pred. No. 1.4e-30;
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US-11-128-900-113
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Best Local Similarity
Matches 48; Conserv
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US-11-128-900-113
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Publication No. US20060021074A1

GENERAL INFORMATION:

APPLICANT: Kellermann, Sirid-Ai

APPLICANT: Green, Larry L.

APPLICANT: Green, Larry L.

APPLICANT: APPLICANT: MOULET

TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION

FILE REFERENCE: ABGENIX 100A2

CURRENT PILING DATE: 2005-03-17

PRIOR APPLICATION NUMBER: PCT/US2005/009306

PRIOR APPLICATION NUMBER: PCT/US2005/009306

PRIOR PELING DATE: 2005-03-17

PRIOR PELING DATE: 2004-03-19

PRIOR PELING DATE: 2004-03-19

PRIOR PELING DATE: 2004-03-19

PRIOR APPLICATION NUMBER: 60/554,372

PRIOR APPLICATION NUMBER: 60/554,372

PRIOR APPLICATION NUMBER: 2004-03-19

NUMBER OF SEQ ID NOS: 266

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 107

TYPE: PRT
                                                                                                                   173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220
                                                                                                                                                           40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
Query Match
18.4%; Score 48; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 48; Conservative 0; Mismatches 0; Indels
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US-11-136-250-107
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173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGGTDFTLKISRVEAED 220

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40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87

Search completed: August 9, 2006, 13:54:56 Job time: 177 secs

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APPLICANT: Larrick, James W. APPLICANT: Larrick, James W. APPLICANT: Integrigen, Inc.
TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses FILE REFERENCE: 021216-0003100S
CURRENT APPLICATION NUMBER: US/11/239,308
CURRENT FILING DATE: 2005-09-28
PRIOR PELING DATE: 2003-10-09
PRIOR PELING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US 60/417,979
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1: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US11_NEW_PUB.pep:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-239-308-2
US-10-239-308-2
US-11-231-902-55
US-11-375-221-111
US-10-497-088-7
US-11-337-300-65
US-11-337-300-65
US-11-337-300-65
US-11-337-300-65
US-11-347-088-14
US-11-249-296-6
US-10-254-182-44
US-11-221-902-49
US-11-21-902-49
US-11-21-902-53
US-11-221-902-54
US-11-221-902-54
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US-11-221-902-54
US-11-221-902-54
US-11-221-902-54
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US-11-221-902-64
US-11-221-902-64
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                                                   - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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seq length: 200000000
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Match Length
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Maximum DB s
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WESUL-123-308-45
; Sequence 45, Application US/11239308
; Sequence 45, Application WS/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Larrick, James W.
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT PILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/11/239,308
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR APPLICATION NUMBER: US 60/417,979
; RIOR APPLICATION NUMBER: US 60/417,979
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NOS : 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.4%; Score 48; DB 7; Length 100; 100.0%; Pred. No. 8.6e-33; ive 0; Mismatches 0; Indels
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US-11-249-296-90
US-11-249-296-90
US-11-291-140-25
US-11-291-140-29
US-11-291-140-47
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US-11-391-140-51
US-11-391-140-51
US-11-311-917-12
US-11-333-104A-21
US-10-533-104A-21
US-10-533-104A-21
US-10-533-104A-21
US-11-337-300-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/11239308
Publication No. US200600888331
GENERAL INFORMATION:
APPLICANT: Smider, Vaughn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 48; Conservative
                     ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
TITLE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT PILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                             Query Match 18.4%; Score 48; DB 7; Length 113; Best Local Similarity 100.0%; Pred. No. 9.4e-33; Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 35; DB 6; Length 247; 100.0%; Pred. No. 1.1e-21; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/10539402
Publication No. US2006011547741
GENERAL INFORMATION:
GENERAL INFORMATION:
THE OF INFORMATION:
TITLE OF INVENTION: OBJECT
TITLE OF INVENTION: OBJECT
TITLE REFERENCE: XEL2EPC
CURRENT APPLICATION NUMBER: US/10/539,402
CURRENT PILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 60/435,893
PRIOR FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: EP 03000615
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PARCHILIN VERSION 3.1
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; Sequence 55, Application US/11221902
; Publication No. US20060086522A1
; GENERAL INFORMATION:
PRIOR FILING DATE: 2002-10-09
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 100.0
Matches 34; Conservative
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                                                                                                       TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-2
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US-11-221-902-55
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Best Local Similarity
Matches 35; Conserva
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ORGANISM: human
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US-10-539-402-18
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LENGTH: 98
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65 QGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

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APPLICANT: Crucell Holland B.V.
APPLICANT: Crucell Holland B.V.
APPLICANT: Cermeraed, Wilfred
APPLICANT: Logtenberg, Ton
APPLICANT: Logtenberg, Ton
APPLICANT: Lekkerkerker, Annemarie N
TITLE OF INVENTION: Presenting cell targeting conjugate, an antigen
TITLE OF INVENTION: Presenting cell contacted with such conjugate, their use for
TITLE OF INVENTION: Generation
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TITLE OF INVENTION NUMBER: POT/FEP01/14255
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
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Best Local Similarity 100.0%; Pred. No. 2.8e-20;
Matches 33; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                      APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: LOW, JOSEPH EDNIN
APPLICANT: MOBLEY, JAMES LESLIE
TITLE OF INVENTION: ANTIBODIES TO M-CSF
FILE REFERENCE: ABX-PF4
CURRENT APPLICATION NUMBER: US/11/375,221
CURRENT FILING DATE: 2006-03-13
PRIOR APPLICATION NUMBER: US/10/938,353
PRIOR APPLICATION NUMBER: 60/502,163
PRIOR FILING DATE: 2003-09-10
                                                                                                                              DEVALARAJA, MADHAV NARASIMHA
FOLTZ, IAN
HAAK-FRENDSCHO, MARY
Sequence 111, Application US/11375221 Publication No. US20060153850Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: FR1 of MatDC16
US-10-497-088-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 117
SOFTWARE: PatentIn Ver. 3.2
                                                                                                  APPLICANT: BEDIAN, VAHE
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TYPE: PRT
ORGANISM: Artificial
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APPLICANT: Crucell Holland B.V.
APPLICANT: Crucell Holland B.V.
APPLICANT: ter Meulen, Jan H.
APPLICANT: ter Meulen, Jan H.
APPLICANT: van den Brink, Edward N.
APPLICANT: Goudsmit, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT FILING DATE: 2006-01-20
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Crucell Holland B.V.
APPLICANT: ter Meulen, Jan H.
APPLICANT: ter Meulen, Jan H.
APPLICANT: van den Brink, Edward N.
APPLICANT: van den Brink, Edward N.
APPLICANT: Soudsmit, Jaap
TITLE OF INVENTION: Binding molecules against SAKS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.9%; Score 31; DB 7; Length 120; Best Local Similarity 100.0%; Pred. No. 1.3e-18; Matches 31; Conservative 0; Mismatches 0; Indels
11.9%; Score 31; DB 6; Length 32; 100.0%; Pred. No. 5e-19; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Variable heavy chain of SC03-012 US-11-337-300-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2e-18;
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Pred. No. 2.2e-1
                                                                                            1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTF 31
                                                                                                                         1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTF 31
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                                                                                                                                                                                                                                                      Sequence 33, Application US/11337300
Publication No. US20060121580A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65, Application US/11337300 Publication No. US20060121580A1
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US-11-337-300-65
                                               31; Conservative
                          Best Local Similarity
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LENGTH: 247
  Query Match
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APPLICANT: ADAMS, GREGORY P.
APPLICANT: HORAK, BVA M.
APPLICANT: HORAK, EVA M.
APPLICANT: WEINER, LOUIS M.
APPLICANT: WEINER, LOUIS M.
APPLICANT: WEINER, LOUIS M.
APPLICANT: WEINER, LOUIS M.
APPLICANT: JAMES, MARKS D.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: US/11/154,103
CURRENT PILING DATE: 2005-06-15
PRIOR PILING DATE: 2005-06-15
PRIOR PILING DATE: 2003-04-02
PRIOR PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 10
LENGTH: 291
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| GENERAL INFORMATION:
| APPLICANT: Crucell Holland B.V. |
| APPLICANT: Germeraad, Wilfred |
| APPLICANT: Logtembergy Ton |
| APPLICANT: Logtembergy Ton |
| APPLICANT: Logtembergy Ton |
| APPLICANT: Logtembergy Ton |
| APPLICANT: Logtembergy Ton |
| APPLICANT: Logtembergy Ton |
| TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen |
| TITLE OF INVENTION: Presenting cell contacted with such conjugate, their use for |
| TITLE OF INVENTION: Qeneration |
| TITLE OF INVENTION: Qeneration |
| TITLE OF INVENTION: Qeneration |
| TITLE OF INVENTION: Qeneration |
| TITLE OF INVENTION UNMBER: US 10/497,088 |
| CURRENT FILING DATE: 2004-06-28 |
| PRIOR FILING DATE: 2002-11-29 |
| PRIOR FILING DATE: 2002-11-29 |
| PRIOR FILING DATE: 2001-12-19 |
| PRIOR FILING DATE: 2001-12-19 |
| PRIOR FILING DATE: 2001-12-19 |
| PRIOR PILING DATE: 2001-12-19 |
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| PRIOR PELING DATE: 2001-12-19 |
| PRIOR PELING DATE: 2001-12-10-10 |
| PRIOR PELING DATE: 2001-12-10-10 |
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| PRIOR PELING DATE: 2001-13-10 |
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LOCATION: (546)..(546)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic antibody. US-11-154-103-10
US-11-154-103-10; Sequence 10, Application US/11154103; Publication No. US20060099205A1
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; Sequence 21, Application US/10497088
; Publication No. US20060088520A1
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US-11-249-296-6
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APPLICANT: Germeraad, Wilfred
APPLICANT: Germeraad, Wilfred
APPLICANT: Germeraad, Wilfred
APPLICANT: Logtenberg, Ton
APPLICANT: Logtenberg, Ton
APPLICANT: Logtenberg, Ton
APPLICANT: Logtenberg, Ton
TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
TITLE OF INVENTION: peneration
TITLE OF INVENTION: generation
TITLE OF INVENTION: generation
TITLE OF INVENTION: generation
TITLE REPRENCE: 0070 US 00 CON
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: PCT/EP01/14255
PRIOR APPLICATION NUMBER: PCT/EP02/13681
PRIOR APPLICATION NUMBER: BC1/EP02/13681
PRIOR FILING DATE: 2002-11-29
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 21
SOUTHARE: Patentin version 3.2
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Publication No. US20060115428A1
GENERAL INFORMATION:
APPLICANT: Schering Aktiengesellschaft
TITLE OF INVENTION: Identification and Characterization of Function-Blocking
TITLE OF INVENTION: AALI-ED-B-Fibronectin Antibodies
FILE REFERENCE: 33042P DE (WWHC)
CURRENT APPLICATION NUMBER: US/11/249,296
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.1
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                                                       11.9%; Score 31; DB 6; Length 1052; 100.0%; Pred. No. 6.5e-18; Live 0; Mismatches 0; Indels
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LOCATION: (836)...(836)
CTHER INFORMATION: Xaa can be any amino acid
US-10-497-088-14
                                                                                                                                                                                                         20 MAQVQLVQSGAEVKKPGASVKVSCKASGYTF 50
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                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 14, Application US/10497088
; Publication No. US20060088520A1
; GENERAL INFORMATION:
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                                                    Query Match 11.9 Best Local Similarity 100. Matches 31; Conservative
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ORGANISM: human
US-10-497-088-21
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APPLICANT: The Government of the United States of America, as APPLICANT: The Government of the United States of America, as APPLICANT: represented by the Secretary of the Department of Health and APPLICANT: Human Services
APPLICANT: Kashmiri, Syed V.S.
APPLICANT: Rashmiri, Syed V.S.
APPLICANT: Badlan, Eduardo A.
TITLE OF INVENTION: MINIMALLY IMMUNGENIC VARIANTS OF SDR-GRAFTED HUMANIZED ANTIBODY TITLE OF INVENTION: CC49 AND THEIR USE
FILE REFERENCE: 4239-6649-03
FILE REFERENCE: 4239-6649-03
FRIOR APPLICATION NUMBER: 05/498,903
FRIOR APPLICATION NUMBER: 65/498,903
FRIOR FILING DATE: 2003-08-29
FRIOR FILING DATE: 2003-08-29
FRIOR FILING DATE: 2004-08-27
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                                                              Gaps
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  Length 117;
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  Score 30; DB 7; L
Pred. No. 8.7e-18;
Query Match 11.5%; Score 30; DB Best Local Similarity 100.0%; Pred. No. 8.7 Matches 30; Conservative 0; Mismatches
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                                                                                                                    3 QVQLVQSGAEVKKPGASVKVSCKASGYTFS 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ANTIBODY FORMULATIONS FILE REFREENCE: P2104R1
CURRENT APPLICATION NUMBER: US/11/254,182
CURRENT FILING DATE: 2005-10-19
PRIOR APPLICATION NUMBER: US 60/620,413
PRIOR FILING DATE: 2004-10-20
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/11254182; Publication No. US20060088523A1; GENERAL INFORMATION:
APPLICANT: ANDYA, JAMES
APPLICANT: GWEE, SHIANG C.
APPLICANT: LIU, JUN
APPLICANT: SHEN, YE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/10570220 Publication No. US20060171941A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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SOFTWARE: Patentin version 3.2
SEQ ID NO 49
LENCTH: 30
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Matches 30, Conservative
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RESULT 15
US-11-221-902-49
US-11-221-902-49
Sequence 49, Application US/11221902
Publication No. US20060088522A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVERTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 04000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT APPLICATION NUMBER: US/11/221,902
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
SOFTWARE: PAT
ORGANISM: Artificial
FEATURE:
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: human antibody sequences
US-11-221-902-49
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                                                         Gaps
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o
Query Match 11.1%; Score 29; DB 6; Length 30; Best Local Similarity 100.0%; Pred. No. 2.2e-17; Matches 29; Conservative 0; Mismatches 0; Indels
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0; Gaps

3 QVQLVQSGAEVKKPGASVKVSCKASGYTF 31

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Search completed: August 9, 2006, 13:55:35 Job time : 34 secs

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Result
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1. FBMC_Celerra_SIDS3/ptodata/2/paa/US066_COMB.pep:*

2. FBMC_Celerra_SIDS3/ptodata/2/paa/US073_COMB.pep:*

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13. FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

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16. FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

17. FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

18. FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

19. FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

11. FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

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18. FBMC_Celerra_SIDS3/ptodata/2/paa/US096_COMB
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/ BMC_CCLEETE SIDS3/ptodata/2/paa/US110_C
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/ BMC_CCLEETE SIDS3/ptodata/2/paa/US111_C
/ BMC_CCLEETE SIDS3/ptodata/2/paa/US112_C
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                                                                                                                                                                                                                                                                                                                                        8366291 seqs, 1526956180 residues
                                                                             - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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seq length: 200000000
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Sequence 2, Appli
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Sequence 7, Appli
Sequence 7, Appli
Sequence 22, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 32, Appl
Sequence 22, Appl
Sequence 22, Appl
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Sequence 59, Appl.
Sequence 11, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 13, Appl.
Sequence 13, Appl.
Sequence 11, Appl.
Sequence 15, Appl.
Sequence 15, Appl.
Sequence 16, Appl.
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1113, App
45, Appl
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82, Appl
75, Appl
107, App
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107428,
23019, A
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107, App
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Match Length I
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ALIGNMENTS

RESULT 1 PCT-USOS-04612-2 Sequence 2, Application PC/TUSOS04612 , GENERAL INFORMATION:

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Query Match
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APPLICANT: Felding-Habermann, Brunhilde
APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Saven, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-0043
CURRENT APPLICATION NUMBER: PCT/USO5/04612
CURRENT FILING DATE: 2005-02-14
PRIOR FILING DATE: 2005-02-14
PRIOR FILING DATE: 2006-02-11
PRIOR PELING DATE: 2004-11-10
PRIOR FILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-11-13
SOFTWARE: PABLICATION NUMBER: US 60/544,807
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 2
LENGTH: 261
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APPLICANT: Pelding-Habermann, Brunhilde
APPLICANT: Janda, Kim D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-0042
CURRENT APPLICATION NUMBER: US/11/056,825
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR PILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/544,807
PRIOR FILING DATE: 2004-11-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.3
SEQ ID NO 2.
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US-11-056-825-2
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PCT-US05-04612-2
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ORGANISM: Artificial
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ORGANISM: Artificial
FEATURE:
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APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Saven, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-0043
CURRENT APPLICATION NUMBER: PCT/USO5/04612
CURRENT FILING DATE: 2005-02-14
PRIOR PELLING DATE: 2005-02-11
PRIOR FILING DATE: 2005-02-11
PRIOR FILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-02-13
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100.0%; Score 261; DB 40; 100.0%; Pred. No. 3.2e-236;
                                                        0; Mismatches
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PCT-US05-04612-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application PC/TUS0504612; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.3
SEQ ID NO 7
                                                     Conservative
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                             Similarity
                                                        261;
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APPLICANT: XENCOR
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ORGANISM: human
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Sequence 7, Application US/11056825
GENERAL INFORMATION:
APPLICANT: Felding-Habermann, Brunhilde
APPLICANT: Fanda, Kinn D.
APPLICANT: Janda, Kinn D.
APPLICANT: Janda, Kinn D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-0042
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR PILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-02-13
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.3
SEQ ID NO 7
LENGTH: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGSGGGSGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Construct
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ORGANISM: Artificial
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Best Local Similarity
Matches 48; Conserv
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TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REPERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT PILING DATE: 2002-05-22
PRIOR PAPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
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APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazarias, John Rudolf
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Desjarlais, Shannon Alicia
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: FP-71386-3 463077-237
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-05-05
NUMBER OF SEQ ID NOS: 184
SOUTWARE: Patentin version 3.2
SEQ ID NO 87
                                                 APPLICANT: Rother, Russell
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: PCT/US02/38450
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
Sequence 22, Application PC/TUS0238450 GENERAL INFORMATION:
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GENERAL INFORMATION:
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Sequence 36, Application US/10153382
GENERAL INFORMATION:
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Matches 48; Conservative
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Best Local Similarity
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40 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
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Best Local Similarity 100.C
Matches 48; Conservative
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Best Local Similarity
Matches 48; Conserv
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US-10-453-698-22
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                                                                                                                                                                                                                                                                                                                SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                            Length 100;
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llarity 100.0%; Pred. No. 3.4e-36;
Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REPRENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                              US-10-308-817-22; Sequence 22, Application US/10308817; Sequence 22, Application US/10308817; SEDERAL INFORMATION: APPLICANT: Rother, Russell
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-36
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 48; Conserva
                                                                                                                                                        Query Match
Best Local Similarity
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; TYPE: PRT
; ORGANISM: human
US-10-308-817-22
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18.4%; Score 48; DB 36; Length 100;
1 Similarity 100.0%; Pred. No. 3.4e-36;
48; Conservative 0; Mismatches 0; Indels
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APPLICANT: Eileen E. Mueller
APPLICANT: Eileen E. Mueller
APPLICANT: Steven C. Gilman
APPLICANT: Steven C. Gilman
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
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APPLICANT: C. Geoffrey Davis
APPLICANT: C. Geoffrey Davis
APPLICANT: Davis
CURRENT APPLICATION NUMBER: US/10/612,497
CURRENT APPLICATION NUMBER: US 09/472087
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFFWARE: Patentin Ver. 2.1
                                                                                APPLICANT: Rother, Russell
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REPRERNCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, BILLEN E.
APPLICANT: HANKE, JEFFREY H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113, Application US/10612497 GENERAL INFORMATION:
US-10-453-698-22; Sequence 22, Application US/10453698; GENERAL INFORMATION:
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173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 220

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APPLICANT: Larrick, James W.
APPLICANT: Integrigen, Inc.
TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
FILE REFERENCE: 021216-00031003;
CURRENT APPLICATION NUMBER: US/10/683,733
CURRENT PILING DATE: 2003-10-09
PRIOR PLILING DATE: 2002-10-09
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 100
TYPE: PRI
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APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/10/612,497A
CURRENT PILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US/09/472,087
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PALCHING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 113
LENGTH: 100
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APPLICANT: Mark J. Neveu
APPLICANT: Eileen E. Wueller
APPLICANT: Eileen E. Wueller
APPLICANT: Steven C. Gilman
APPLICANT: C. Geoffrey Davis
APPLICANT: JESE R. COTVALAN
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFL DIV2
CURRENT APPLICATION NUMBER: US/10/776,649
CURRENT FILING DATE: 2004-02-10
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US-10-683-733-45
Sequence 45, Application US/10683733
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 48; Conserv
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US-10-776-649-113
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Sequence 87, Application US/11332619
GENURAL INFORMATION:
APPLICANT: Mores, Gregory L.
APPLICANT: Marshall, Shannon Alicia
TITLE OF INVENTION: ANTIBODIES AND FC FUSION PROTEINS WITH ALTERED IMMUNOGENICITY
FILE REFERENCE: 18750/US/4 463077-427
CURRENT APPLICATION NUMBER: US 60/643,313
PRIOR APPLICATION NUMBER: US 60/63,313
PRIOR APPLICATION NUMBER: US 60/652,958
PRIOR FILING DATE: 2005-01-12
RIOR APPLICATION NUMBER: US 60/652,958
PRIOR FILING DATE: 2005-02-14
PRIOR FILING DATE: 2005-02-14
PRIOR FILING DATE: 2005-02-14
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Sequence 87, Appl
Sequence 38, Appl
Sequence 12, Appl
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1. /EMC_Celerra_SIDS3/ptodata/2/paa/PCT_NEW_COMB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/2/paa/US06_NEW_COMB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/2/paa/US07_NEW_COMB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/2/paa/US09_NEW_COMB.pep:*

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5. /EMC_Celerra_SIDS3/ptodata/2/paa/US10_NEW_COMB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/2/paa/US10_NEW_COMB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/2/paa/US11_NEW_COMB.pep:*

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                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REPERENCE: 30219/US/S.
FILE REPERENCE: 30219/US/S.
CURRENT PILING DATE: 2006-05-10
FRIOR PELLORTION NUMBER: US/11/432,734
CURRENT FILING DATE: 2006-05-10
FRIOR PELLORTION NUMBER: US/11/054,669
FRIOR FILING DATE: 2005-02-08
FRIOR PELLORTION NUMBER: US 10/194,975
FRIOR FILING DATE: 2002-07-12
FRIOR PELLORTION NUMBER: US 60/305,111
FRIOR FILING DATE: 2001-07-12
FRIOR FILING DATE: 2001-07-12
FRIOR FILING DATE: 2010-07-12
FRIOR FILING DATE: 2010-07-13
FRIOR PELLORTION NUMBER: US 60/305,111
FRIOR FILING DATE: 2010-07-13
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Best Local Similarity 100.
Matches 48; Conservative
                          ; ORGANISM: Homo sapiens
US-11-432-734-75
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APPLICANT: HANSEN; HANS J.
APPLICANT: HEUNG, SHUI-ON
APPLICANT: USUNG, SHUI-ON
APPLICANT: QU, ZHENGXING
APPLICANT: QU, ZHENGXING
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: INTERNALIZING ANTI-CD-74 ANTIBODIES AND METHODS OF USE
TILE REPERENCE: 78258/329656
CURRENT APPLICATION NUMBER: US/10/377,122
CURRENT FILING DATE: 2003-03-03
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 36
SOOTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                      0; Indels
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US-11-346-403A-38
                                                                                                                                                                                        Score 48; DB 7; L. Pred. No. 2.4e-37;
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APPLICANT: Schoonbroodt, Sonia
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: LIBRARIES AND METHODS FOR
TITLE OF INVENTION: ISOLATING ANTIBODIES
FILE REPERENCE: 10280-116001
CURRENT APPLICATION NUMBER: US, 2006-02-01
PRIOR APPLICATION NUMBER: US, 60/649,065
PRIOR FILING DATE: 2005-02-01
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100.0%; Pred. No....
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 103
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8-11-346-403A-38
5 Sequence 38, Application US/11346403A
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 1939
SOFTWARE: PatentIn version 3.3
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                           Best Local Similarity 100.
Matches 48; Conservative
                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-332-619-87
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Matches 48; Conserva
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SEQ ID NO 12
LENGTH: 111
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                                                  SEQ ID NO 87
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Sequence 1964, Application US/60815559

Sequence 1964, Application US/60815559

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITIE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REPERENCE: PF233P913

CURRENT APPLICATION NUMBER: US/60/815,559

CURRENT FILING DATE: 2006-06-22

SURMER OF SEQ ID NOS: 3247

SEQ ID NO 1964

LENGTH: 253
                                                                                                                                                                                                           Sequence 1964, Application US/60797351
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REFERENCE: PF523P911
CURRENT APPLICATION NUMBER: US/60/797,351
CURRENT PILING DATE: 2006-05-04
SEQ ID NOS: 3247
LENGTH: 253
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REPERENCE: PF523PP12
FURENT APPLICATION NUMBER: US/60/814,869
CURRENT FILING DATE: 2006-06-20
NUMBER OF SEQ ID NOS: 3247
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  100.0%; Pred. No. 2.6e-37; ive 0; Mismatches 0;
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GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 48; Conservative
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CRGANISM: Homo sapiens
US-60-815-559-1964
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US-60-797-351-1964
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Best Local Similarity
Matches 48; Conserv
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REFERENCE: PF523PP13
CURRENT APPLICATION NUMBER: US/60/815,559
CURRENT FILING DATE: 2006-06-22
NUMBER OF SEQ ID NOS: 3247
LENGIH: 246
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REFERENCE: PF523P914
CURRENT APPLICATION NUMBER: US/60/834,152
CURRENT FILING DATE: 2006-07-31
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1192
LENGTH: 246
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
TITLE PEPERBOCE: PF523PP11
CURRENT PAPLICATION NUMBER: US/60/797,351
CURRENT FILING DATE: 2006-05-04
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3242
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                                                                     Query Match
14.9%; Score 39; DB 8; L
Best Local Similarity 100.0%; Pred. No. 1.3e-28;
Matches 39; Conservative 0; Mismatches 0;
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14.9%; Score 39; DB 8; La
Best Local Similarity 100.0%; Pred. No. 1.3e-28;
Matches 39; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-60-814-869-1192
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CRGANISM: Homo sapiens
US-60-834-152-1192
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US-60-815-559-1192
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US-60-797-351-3242
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Best Local (
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato FILE REFERENCE: PF523PP11
CURRENT APPLICATION NUMBER: US/60/797,351
CURRENT FILING DATE: 2006-05-04
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1192
LENGTH: 246
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato FILE REPERENCE: PF523PP14 CURRENT APPLICATION NUMBER: US/60/834,152
CURRENT FILING DATE: 2006-07-31
NUMBER OF SEQ ID NOS: 3247
LENGTH: 253
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Sequence 1192, Application US/60814869

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulatc

FILE REFERENCE: PF523PP12

CURRENT APPLICATION WUMBER: US/60/814,869

CURRENT FILING DATE: 2006-06-20

NUMBER OF SEQ ID NOS: 3247

LENGTH: 246
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                        Query Match 18.4%; Score 48; DB 8; Length 253; Best Local Similarity 100.0%; Pred. No. 5.5e-37; Matches 48; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Conservative
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Best Local Similarity
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RESULT 14
US-60-814-869-3242
i Sequence 3242, Application US/60814869
c Sequence 3242, Application US/60814869
c GENERAL INFORMATION:
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulate;
    TILE REPERENCE: PFS.22PP12
    CURRENT APPLICATION UNDBER: US/60/814,869
    CURRENT FILING DATE: 2006-06-20
    NUMBER OF SEQ ID NOS: 3247
    SEQ ID NO 3242
    LENGTH: 247
    TYPE: PRT
    TYPE: PRT
    CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ruben et al.
TITLE OF INVENTION: Autibodies that Immunospecifically Bind to B Lymphocyte Stimulato FILE REPERENCE: PF523PP13
CURRENT APPLICATION NUMBER: US/60/815,559
CURRENT FILING DATE: 2006-06-22
SEQ ID NOS: 3247
LENGTH: 247
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                                                                                                                ch 14.2%; Score 37; DB 8; Length 247; 1 Similarity 100.0%; Pred. No. 9.7e-27; 37; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                   62 QKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98
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Job time : 36 secs
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ORGANISM: Homo sapiens
US-60-815-559-3242
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-797-351-3242
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Matches 37; Conserva
                                                                                                                          Query Match
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9, 2006, 13:34:32 ; Search time 39 Seconds August Run on:

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643.912 Million cell updates/sec

US-11-056-825-2

score:

1 MAQVQLVQSGAEVKKPGASV......KVEIKRGLGGLVDYKDDDDK 261 Sequence:

Scoring table:

283416 seqs, 96216763 residues OLIGO Gapop 60.0 , Gapext 60.0 Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	& Query Match	Length	DB	SUMMARIES	Description
1	48	18.4	114	8	849572	Iq kappa chain pre
7	48		114	7	B49002	chain
m	48	18.4	120	7	S42268	ь
4	48	18.4	133	Н	A24452	g kappa
2	48	18.4	133	Н	K2HURP	g kappa chain
9	48	18.4	133	~	S23230	chain
7	48	18.4	133	~	S42611	UNVK protein p
80	48	18.4	142	~	822902	kappa chair
6	37	14.2	122	7	S40338	
10	35	13.4	129	7	S36260	
11	34	13.0	96	~	S26919	
12	34	13.0	131	7	S21924	heavy
13	33		122	7	S36271	heavy
14	33	12.6	132	0	S40322	
15	32	12.3	118	7	S40374	kappa
16	32	12.3	124	~	S19665	Ig heavy chain V r
17	32	12.3	140	7	S22658	kappa chain
18	29	11.1	98	N	526920	
19	29	11.1	98	7	S26918	heavy
20	29	11.1	98	N	S26912	
21	29	11.1		7	S26938	heavy
22	29	11.1	96	~	S26913	
23	29	11.1	104	N	869899	heavy
24	29	11.1	111	7	S21925 .	
25	53	11.1	116	N	S31667	heavy
26	29	11.1	117	н	HVHU35	heavy
27	29	11.1	117	н	HVHUHG	heavy chain
28	29	11.1	117	~	S18552	heavy chain
29	29	11.1	117	~	S31680	Ig heavy chain V r

Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r	heavy heavy i-Sm	ig neavy chain v r Ig heavy chain v r Ig kappa chain v r Ig kappa chain v r	Ig kappa chain V r Ig kappa chain V-J Ig kappa chain V r	Ig kappa chain V r Ig light chain V r Ig kappa chain V r
S18553 S18551 S36265	\$46393 \$31596 \$49530	A32483 S29257 S42267 S34093	H30538 S40337 S34094	S34091 PH1039 PL0258
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30 31 32	1 W W W V	9 K B B 6 B B B	4 4 4 0 1 6	4 4 4 6 4 3

ALIGNMENTS

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A,Accession: S49572
A,Status: preliminary
A,Molecule type: mRIAA
A,Residus: 1-114 <GIAA
A,Residus: 1-114 <GIAA
C,Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                      C,Accession: S49572
R,Giachino, C.; Padovan, E.; Lanzavecchia, A.
submitted to the EMBL Data Library, November 1994
A;Description: k+1+ dual receptor B cells are present in the human peripheral repertoire.
A;Reference number: S49571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                     C;Species: Homo sapiens (man)
C;Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
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Ig kappa chain precursor - human (fragment)
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Ig kappa chain V region, rheumatoid factor RF antibody - human (fragment) C;Species: Homo sapiens (man) C;Species: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C; Accession: B49002

Ristuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.; Arthritis Rheum. 35, 900-904, 1992
A; Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene A; Reference number: A49002; MUID:92352481; PMID:1322670

A; Accession: B49002

A;Status: preliminary A;Molecule type: mRNA

A; Residues: 1-114 <STU>

A;Cross-references: UNITROT:09UL80; UNIPARC:UP10000176B43
A;Experimental source: EBV-transformed lymphoblastoid cell line SSH23
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:110263, NCBIP:110264)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Gaps ; 0 18.4%; Score 48; DB 2; Length 114; 100.0%; Pred. No. 1.6e-36; Live 0; Mismatches 0; Indels Query Match Best Local Similarity 100.(Matches 48; Conservative

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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar C;Superfamily: immunoglobulin V region; immunoglobulin homology (C;Keywords: heterotetramer; immunoglobulin E;1-20/Domain: signal sequence #status predicted <SIG>P;21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
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A;Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and ligh
A;Reference number: S23230; MUID:91178438; PMID:1840606
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                                  C'Species: Homo sapiens (man)
C'Accession: 401-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C'Accession: Aun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
R'Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nucleac Acids Res. 13, 6499-6513, 1985
A;Title: Human immunoglobulin kappa light chain genes of subgroups II and II.
A;Reference number: A93588; MUID:86041852; PMID:2997711
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P06310; UNIPARC:UPI000012E159
A;Note: the sequence was determined from the differentiated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 133;
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C;Superfantly: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>
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100.0%; Pred. No. 1.8e-36;
ive 0; Mismatches 0;
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Ig kappa chain precursor V-II region (RPMI) - human
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;36-115/Domain: immunoglobulin homology <IMM>
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F;60-74/Region: framework 2
F;75-81/Region: complementarity-determining 2
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A;Map position: 2p12-2p12
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Best Local Similarity
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:IGKV2
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                                                                                                                                                                                                                             Ig kappa chain V region (Al7) - human (Species: Homo sapiens (man) (5pecies: Homo sapiens (man) (5pecies: Homo sapiens (man) (5pate: 3) - Apr-1999 #sequence_revision 30-Apr-1999 #text_change 31-Dec-2004 (5) - Accession: 542268 (S. A.) Huber, C.) Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zchautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zchautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zchautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Thiebe, R.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rieske, A.; Zchautner-Rie
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A,Note: this sequence was determined from the differentiated gene
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R;Weir, L.; Leder, P.
Nucleic Acids Res. 14, 3957-3970, 1986
A;Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
A;Reference number: A24452; MUID:86232631; PMID:3086847
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;21.133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
;36-115/Domain: immunoglobulin homology <IMM>
;43-113/Disulfide bonds: #status predicted
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;Species: Homo sapiens (man)
;Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
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Cross-references: UNIPROT:Q8TCD0, UNIPARC:UP10000176EB9; EMBL:X63403
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40 WFQQRPGQSPRLIXKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.4%; Score 48; DB 2; Length 120; Best Local Similarity 100.0%; Pred. No. 1.6e-36; Matches 48; Conservative 0; Mismatches 0; Indels
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C;Superfamily: immunoglobulin homology
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A;Cross-references: GDB:136265
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Matches 48; Conserv
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A; Residues: 1-133 <WEI>
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C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; EMBO J. 12, 725-734, 1993
A;Title: Malmanti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Referession: S36260
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C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology < MM>
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
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J. Mull. Biol. 227, 776-798, 1992
J. Mull. Biol. 227,
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C;Species: Homo sapiens (man)
C;Date: 03-Peb-1994 #sequence_revision 03-Peb-1994 #text_change 23-Jul-1999
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
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                                                                                     Score 37; DB 2; Lengtn 122.
Pred. No. 2e-26;
0; Indels
                                                                                                                          Length 122;
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                                                                                                                  Query Match 14.2%; Score 37; DB Best Local Similarity 100.0%; Pred. No. 2e-Matches 37; Conservative 0; Mismatches
C; Keywords: heterotetramer; immunoglobulin P; 22-101/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 100.0
Matches 35; Conservative
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Best Local Similarity
Matches 34; Conserv
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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A;Residues: 1-133 <2FA>
A;Cross-references: UNIPARC:UPI000011378B; EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                         C;Accession: S42611
R;Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.
Neuroimmunol. 36, 29-39, 1992
A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regingle A;Reference number: S42610; WUID:92138794; PMID:1370957
A;Accession: S42611
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A,Reference number: S22902; MUID:91276289; PMID:1905262
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A,Residues: 1-122 <KLE>
A,Cross-references: UNIPARC:UPI0000116158; EMBL:X72448; NID:g441364; PIDN:CAA51116.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
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Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
Accession: S22902
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C;Spacies: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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A;Cross-references: UNIPARC:UPI0000176CAB; EMBL:X56510
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 1.9e-36;
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Gene 101, 305-306, 1991
                                                                                                                                                               protein precursor - human
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Matches 48; Conserv
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A;Residues: 1-118 <KLE>
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A;Cross-references: UNIPARC:UPI0000118DE3; EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < NMV>
                                                                                                                                                                                    A;Residues: 1-111 <FRI>
A;Cross-references: UNIPARC:UP10000115FA2; EMBL:X60505; NID:g33565; PIDN:CAA43025.1; PID
C;Genetics:
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S4032
R;Klein, R:, Jaenichen, R:, Zachau, H.G.
Bur. J: Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C'Species: Homo sapiens (man)
C'Date: 03-Peb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                       C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
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A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
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Pred. No. 1.2e-23;
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C.Accession: S21924, S21923
R.Friedman, D.F.
submitted to the EMBL Data Library, July 1991
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A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
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Matches 33; Conservative
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A; Status: preliminary
A; Molecule type: DNA
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Best Local S:
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S40322
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
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                                                                            74 KVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED 106
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         0; Mismatches
                                                  188 KVSNRDSGVPDRFSGSGSGTDFTLKISRVEAED
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C;Keywords: heterotetramer; immunoglobulin
F;20-99/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 100.0
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Myosin-reactive immunoglobulin light chain variable region (Fragment).
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Q60091_HUMAN
Q96QSO_HUMAN
HV1B_HUMAN
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92289816; PubMed=1601042;
Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                      MEDLINE=92352481; PubMed=1322670; Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr, Gaskin F., Fu S.M.; "A rheumatoid factor from a normal individual encoded by VH2 and V
                                                                                                                                                                                                                                                                                    "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                             MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                            fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                       V kappa-J kappa coding joint.";
Eur. J. Immunol. 22:1561-1565(1992).
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PIR; B49002; B49002.
PIR; S23638; S23638.
                                                                                                                                                                                                                                                                                                                      Eur. J. Immunol. 23:391-397(1993).
                                                                                                                                                                                                                    kappa II gene segments.";
Arthritis Rheum. 35:900-904(1992)
                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
MEDLINE=93170387; PubMed=8436174;
Wagner S.D., Luzzatto L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, S34094, S34094.
PIR, S34095, S34095.
HSSP, P01625, 1LVE.
SWR, Q9UL80, 1-114.
InterPro; IPR003599, IG.
InterPro; IPR003599, IG.
InterPro; IPR003596, IG-V.
InterPro; IPR013106, V-Bet.
SWART; SM00406, IG', 1.
FROSITE; PSS90835, IG_LIKE; 1.
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KV2F HUMAN ID KV2F HUMAN STANDARD; PRT; 133 AA. AC P063IO; DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.

RESULT 3

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                                                             Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                         MEDLINE-86041852; PubMed-2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V-II region RPMI 6410.
/FTId=PRO_0000015173.
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Immunoglobulin domain; Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003923; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR003599; IG. InterPro; IPR003599; IG. V: InterPro; IPR003596; IG. V: InterPro; IPR013106; V-set. Fam; PF05666; V-set. SMART; SM00406; IG; I. SMART; SM00406; IG; I.
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07-MAR-2006, entry version 41.
Ig kappa chain V-II region RPMI 6410 precursor.
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PIR; A01890; K2HURP.
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SMR; PG6510, 21-133.
Ensembl; RNSG00000173758; Homo sapiens.
LinkHub; P06310; --.
                                                                                                                                                                                                                                                                                Nucleic Acids Res. 13:6499-6513(1985).
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                                                Straubberg R.L., Feingold E.A., Grouse L.H., O'spanial Straubberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D., Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altaeher S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Stapleron M., Soares M.B., Bonaldo M.F., Casrunici P., Frange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Schwultz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schmitz M., Marra M.A.; Schnerch A., Schmitz J., Myers R.M., Schnerch A., Schmitz J., Marra M.A.; Railus D.E., Grenztion and initial analysis of more than 15,000 full-length human
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Klein R., Jaendichen R., Zachau H.G.;
"Expressed human immunoglobulin kappa genes and their hypermutation.";
Eur. J. Immunol. 23:3248-3262(1993).
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MEDLINE=91170987; PubMed=8436174;
MEDLINE=91170987; PubMed=8436174;
Magner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are
"V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirabayashi Y., Mumakata Y., Sasaki T., Sano H.;
"Variable regions of a human anti-DNA antibody O-81 possessing lupus
nephritis-associated idiotype.";
Nucleic Acids Res. 20:2601-0(1992).
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Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,
Thiebe R., Zocher I., Zachau H.G.;
"The human immunoglobulin kappa locus. Characterization of the
                           TISSUE-Lung;
MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC022362; AAH22362.1; -; mRNA.
PIR; S22658; S22658.
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InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
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PIR, S40324; S40324.
PIR, S40374; S40374.
PIR, S42267; S42267.
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      somatic mutation.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                     Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R EMBL; BK640625; CAE45779.1; -; mRNA.

R HSSP; P01751; 1A6W.

R InterPro; 1PR001359; 1G-11ke.

R InterPro; 1PR001359; 1g_-c1.

R InterPro; 1PR001359; 1g_-c1.

R InterPro; 1PR001306; 1g_-WHC.

R InterPro; 1PR001306; 1g_-WHC.

R InterPro; 1PR0013106; V-set.

R SMART; SM00409; 1G; 1.

SMART; SM00400; 1G4; 1.

SMART; SM00400; 1G-1; 2.

R PROSITE; PS50835; 1G_LIKE; 4.

R PROSITE; PS50835; 1G_LIKE; 4.

R PROSITE; PS00290; 1G_MHC; Immunoglobulin domain; Repeat.

NON_TER
                                                                                        PEGNITY PROTEST, CL. Set, 1.
SWART; SW00409; IG; 1.
SWART; SW00406; IG: 1.
SWART; SW00406; IG: 1.
PROSITE; PS50835; IG_LIKE; 2.
HYDOTHELICAL protein.
HYDOTHELICAL protein.
SEQUENCE 239 AA; 26235 MW; PACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           60 WFQQRPGSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 AA; 54160 MW; 3C423A17D65A41B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  173 WPQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 2; Le
Pred. No. 3.2e-22;
                                                                                                                                                                                                                                                                                                                   Score 41; DB 2; Losted. No. 4.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 12. Hypothetical protein DKPZp686C02220 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 QGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCA 134
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                                                                                                                                                                                                                                                                                                 15.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The German Human cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR013106; V-Bet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rISSUE=Human rectum tumor;
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=DKFZp686C02220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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LinkHub; P01743; -.
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117
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SEQUENCE
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DOR REPORT THE SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOLUTION OF SOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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21-JUL-1986, sequence version 1.
07-MAR-2006, entry version 41.
119 heavy chain V-I region HG3 precursor.
Homo sapiens (Human).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tilson M.D.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
                                                                                                       QGGSO HUMAN PRELIMINARY; PRT; 159 AA. 096080.
096080.
01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
21-FEB-2006, entry version 20.
Putative matrix cell adhesion molecule-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Preq. ...
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PIR; A02024; HVHUHG.
HSSP: P01751; INOB.
SMR; P01743; 20-117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY039025; AAK82649.1; -; mRNA.
HSSP; P01869; 1AE6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003599; Ig.
Interpro; IPR007110; Ig-like.
Interpro; IPR013596; Ig-v.
Interpro; IPR013106; V-Eet.
SMART; SM00409; IG; I.
SMART; SM00406; IG-V: I.
PROSITE; PS50835; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                       HUMAN
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HV1B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                     RESULT 6
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93209281; PubMed-7681398; Mariette X., Tsapis A., Brouet J.C.; Mariette X., Tsapis A., Brouet J.C.; Molistic Sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88296408; Pubmed=2841108; Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q., Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q., Dhon H., Fukuhara S., Honjo T.; In the human immunoglobulin heavy-chain locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Immunol. 23:846-851(1993).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V-I region HG3.
/FTId=PRO_000015244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR0013106; V-set.
InterPro; IPR0016; V-set.
InterPro; IPR0066; V-set.
InterPro; SMOART; SMOAG66; IG-V:
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X07448; -; NOT_ANNOTATED_CDS; Genomic_DNA. PIR; S00476; HVHU35.
HSSP; P01751; 1NQB.
SMR; P23083; 20-117.
Ensembl; ENSG00000130076; Homo sapiens.
LinkHub; P23083; -.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005576; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; V-Set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1991, integrated into UniProtKB/Swiss-Prot. 01-NOV-1991, sequence version 1. 07-MAR-2006, entry version 36. 617 heavy chain V-I region V35 precursor. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 29; DB 1; Le 100.0%; Pred. No. 5.3e-19; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 20-116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QVQLVQSGAEVKKPGASVKVSCKASGYTF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 OVOLVOSGAEVKKPGASVKVSCKASGYTF 48
                                                                                                                                                                                                                                                                                                                                                                                                       Ig-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Local 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 7:1047-1051 (1988).
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CHAIN

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Matches

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                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                              patient with plasma cell dyscrasia and amyloidosis.",
J. Clin. Invest. 52:1276-1281(1973).
-!- MISCELLANBOUS: The major amyloid protein appears to be identical
with the Bence Jones protein isolated from the same patient.
-!- MISCELLANBOUS: This protein was isolated from the urine of a
patient with plasma cell dyscrasia and amyloidosis.
-!- MISCELLANBOUS: The C region of this chain has the INV (1,2)
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=73166638; PubMed=4700495;
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Glenner G.G.;
"Structural identity of Bence Jones and amyloid fibril proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO: Uv. ...

GO; GO: 0006955; P: 1mm.

R InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

DR InterPro; IPR003596; Ig.

DR InterPro; IPR003596; Ig.

DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IG; 1.

DR SMART; SM00406; IG; 1.

DR SMART; SM00406; IG.

RW Amyloid; Bence-Jones protein; Direct protein sequencing;

KW Amyloid; Bence-Jones protein; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin V-II region TEW.

Ig kappa chain V-II region TEW.

/ Framework-1.

Pramework-1.

Pramework-1.

Pramework-2.
                                                                                                                                                                                                                              MEDLINE=74146480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12316 MW; 0C3C38F81F1843CA CRC64;
                                   21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 21-JUL-1986, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 27; DB 1; Le llarity 100.0%; Pred. No. 4.1e-17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW). MEDLINE=73166638; PubMed=4700495;
   113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE (BENCE-JONES PROTEIN TEW).
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   PRT;
                                                                                                                                                                                                                                                                                         primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
                                                                      07-MAR-2006, entry version 45.
Ig kappa chain V-II region TEW.
Homo sapiens (Human).
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A90370; K2HUTW.
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94
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113 AA;
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                                                                                                                                                                             NCBI_TaxID=9606;
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Best Local Simi
Matches 27;
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   KV2D HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; "The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                      Gaps
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                                                                                        Ig heavy chain V-I region V35. /FTId=PRO_000015245.
                                                                                                                                                                                               11.1%; Score 29; DB 1; Length 117; 100.0%; Pred. No. 5.3e-19; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 27; DB 2; Length 112; 100.0%; Pred. No. 4.1e-17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
Pfam; PF07686; V-set; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                              117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AA; 12270 MW; C844B7881A89C18A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 07-FBB-2006, entry version 4. Kappa chain (Fragment).
                                                                                                                                                                                                                                                                       3 QVQLVQSGAEVKKPGASVKVSCKASGYTF 31
                                                                                                                                                                                                                                                                                           20 QVQLVQSGAEVKKPGASVKVSCKASGYTF 48
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                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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InterPro; IPR003599; IG.
InterPro; IPR003596; Ig-1; InterPro; IPR003596; Ig-v.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
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NUCLEOTIDE SEQUENCE OF 108-109.
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                    29; Conservative
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117 117
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                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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SEQUENCE
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MOUSE
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Gaps

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61 SGVPDRFSGSGSGTDFTLKISRVEAED 87

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KV2D_HUMAN RESULT 10

Length 113;

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61 SGVPDRFSGSGSGTDFTLKISRVEAED 87
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InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-like.
InterPro; IPR003596; Ig v.
InterPro; IPR013106; V-8et.
SNAAT; SM04009; IG; 1.
FNART; SM04006; IG; 1.
FNOSITE; PSS0835; IG_LIKE; 1.
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                                                                                    Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
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NON_TER 1 1
NON_TER 115 115
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Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erlandsson A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diversity."
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ID KV2E HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                          21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
21-JUL-1986, sequence version 1.
07-MAR-2006, entry version 39.
Ig kappa chain V-II region 26-10.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novotny J., Margolies M.N.;
"Annino acid sequence of the light chain variable region from a mouse anni-digoxin hybridoma annibody.";
Biochemistry 22:1153-1158 (1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
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InterPro; IPR003599; Ig.

InterPro; IPR003110; Ig-1-like.

InterPro; IPR003166; V-set.

InterPro; IPR013106; V-set.

InterPro; IPR07686; V-set.

InterPro; IPR0406; Ig. 1.

InterPro; IPR0406; Ig. 1.

InterPro; IPR0406; Ig. 1.

InterPro; IPR0406; Id. 1.

InterPro; IPR0406; Id. 1.

InterPro; IPR05116; V-set.

InterPro; IPR05116; V-set.

InterPro; IPR05116; Id. 1.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

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InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

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InterPro; IPR05116; Id. II.

InterPro; IPR05116; Id. II.

Int
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/FTId=PRO 0000059776.
Framework-1.
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Pred. No. 4.1e-17;
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113
12273 MW; F9F39CE949A84C2A CRC64;
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15-WAR-2005, sequence version 1.
07-FBB-2006, entry version 6.
Kappa light chain variable region (Fragment).
Name-1gGl anti-TS1 VL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Sco...
100.0%; Pred. No.....
0; Mismatches
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Ensembl; ENSMUSG0000055315; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Framework-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A/J;
MEDLINE=83178921; PubMed=6404298;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein that binds digoxin.
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AC Q5F2IO, AC G5F2IO;
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                                                                                                                           STANDARD;
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62
94
103
23
113 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE.
                                                                                                                           KV2G MOUSE
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SEQUENCE
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                                                                                                                                                                                        [1] —
NUCLBOTIDE SEQUENCE.
NUCLBOTIDE SEQUENCE.
MEDIAME=22716456; PubMed=12833571; DOI=10.1002/jmr.617;
Exlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
Exlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
"Studies of the interactions between the anticytokeratin 8 monoclonal antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";
J. Mol. Recognit. 16:157-163(2003).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=84191506; PubMed=6125927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erianusson A.;
Submitted (FBB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z00009; -; NOT ANNOTATED CDS; Genomic_DNA.
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HSSP; Q99M37; 1191.
SMR; P06309; 5-115.
LinkHub; P06309; -:
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Balb/c; TISSUE-Spleen; MEDLINE=96319505; PubMed=8768802; Kipp B., Schlaak M., Becker W.M.; "Cloning and expression of a recombinant mouse Fab-fragment recognizing a defined linear epitope of Chironomus thummi thummi major allergen Chi t I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                 Ig kappa chain V-II region GM607./FTId=PRO_0000015172.
                                                                                                                                                                     Complementarity-determining-1.
                                                                                                                                                                                             Complementarity-determining-2.
                                                                                                                                                                                                          Framework-3.
Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                    Score 27; DB 1; Length 117;
Pred. No. 4.2e-17;
                                                                                                                                                                                                                                                                                                                             0; Indels
      InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003100; Ig-like.
InterPro; IPR003106; V-Set.
Fiam; PP07686; V-Set.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
SIGNAL.
                                                                                                                                                                                                                                                                                12664 MW; 92C57DC719E558B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nt. Arch. Allergy Immunol. 110:348-353(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                          219 AA.
                                                                                                                                                                                                                                                                                            Match 10.3%; Score 27; up Local Similarity 100.0%; Pred. No. 4.2
                                                                                                                                                                                                                                             By similarity
                                                                                                                                                                                Framework-2.
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                                                                                                                                                                                                                                                                                                                                                                   65 SGVPDRFSGSGSGTDFTLKISRVEAED 91
30; GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2004, sequence version 1.
07-FBB-2006, entry version 12.
Kappa light chain C_region (Fragment).
Name=1gk-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                      QESZCO_MOUSE PRELIMINARY; PRT;
QESZCO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z37499; CAA85724.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI, MGI:96495, IGK-C.
InterPro; IPR003599, IG.
InterPro; IPR003109, IG-118.
InterPro; IPR003109, IG-118.
InterPro; IPR003106, IG-NGC.
InterPro; IPR013106, V-8et.
Pfam; PF07654; CI-8et; 1.
SMART; SM00407; IG-1; 1.
SMART; SM00407; IG-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                  117 1
117 AA;
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RETAINSEZECH II, TISSUE-Mammary tumor metastatized to lung.

RETAINSEZECH II, TISSUE-Mammary tumor metastatized to lung.

MULTIPSECH II, TISSUE-Mammary tumor metastatized to lung.

MEDLINE-2238627; PubMed-12477932; DOI-10.1073/pnas.242603899;

Strausberg R.L., Feingold B.A., Grouse L.H., Derge G.G.,

Alsenis R.E., Zeberg B.A., Buerow K.H., Schemen C.M., Schuler G.D.,

Alsenis R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Woßwan P.J., McKernan K.J., Malke J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Loquellano N.A., Peters G.J., Dickson M.C.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A. C., Grimmood B., Sanchez A.,

Mhiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roche R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Roche R. Schnerch B. Schein J.E., Jones S.J.M., Marra M.A.;

Roch M., Soche R. S., Garcia B. S., Sanchez B. D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roch M. Schein J.E., Jones S.J.M., Marra M.A.;

Roch M. Schnerch A., Schein J.E., Jones B.J.M., Marra M.A.;

Roch M. Schein J.E., Jones B.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Igk-C;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung.
MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR enhancer.;
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                                                                                                                                                                Query Match 10.3%; Score 27; DB 2; Length 219; Best Local Similarity 100.0%; Pred. No. 7.6e-17; Matches 27; Conservative 0; Mismatches 0; Indels
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                                                                                                                   219 AA; 23945 MW; 7E1B82A14EAF8445 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z6-APR-2005, integrated into UniProtKB/TrEMBL. 26-APR-2005, sequence version 1. 07-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                         239 AA.
                                                                                                                                                                                                                                                                    194 SGVPDRFSGSGSGTDFTLKISRVEAED 220
                                                                                                                                                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVEAED 87
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MGI; MGI:96495; Igk-C.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig.
InterPro; IPR003697; Ig.
InterPro; IPR003696; Ig.
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                    PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Repeat.
NON_TER 1 219
SEQÜENCE 219 AA; 23945 MW;
PROSITE; PS50835; IG LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR013106; V-set.
SMART; SM00409; IG; 1.
SMART; SM00407; IG; 1.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 239 AA; 26302 MW; 98FC4BA8EB404215 CRC64;
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Query Match 10.3%; Score 27; DB 2; Length 239; Best Local Similarity 100.0%; Pred. No. 8.2e-17; Matches 27; Conservative 0; Mismatches 0; Indels ઠે q

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0; Gaps

Search completed: August 9, 2006, 13:39:20 Job time : 302 secs

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1 MAQVQLVQSGAEVKKPGASV......KVEIKRGLGGLVDYKDDDDK 261
                                                                                                               9, 2006, 13:05:47; Search time 195 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

	Description	Aec92007 Single ch	Abp45953 Human BLy	Adg96780 Single ch		Aay21884 Amino aci	Adp03811 Human ant	Aab70171 Recombina	Aau90900 Insulin/i	Aea44228 Anti-TPO	Aee02143 Anti-Mpl	Aec92009 Single ch	Aea44222 Anti-TPO	Aee02142 Anti-Mpl	Aea43937 Anti-TPO	Aee02103 Anti-Mpl	Adp03813 Human ant	Aea44195 Anti-TPO	Aee02107 Anti-Mpl	Aea44189 Anti-TPO	Aee02105 Anti-Mpl	Aab23817 Plasmid p	Aag67493 Amino aci	Aam47631 Murine MA
SUMMARIES	ID	AEC92007	ABP45953	ADG96780	AED78833	AAY21884	ADP03811	AAB70171	AAU90900	AEA44228	AEE02143	AEC92009	AEA44222	AEE02142	AEA43937	AEE02103	ADP03813	AEA44195	AEE02107	AEA44189	AEE02105	AAB23817	AAG67493	AAM47631
	DB	9	ഗ	7	σ	7	Φ	4	Ŋ	σ	6	6	σ	σ	σ	σ	œ	σ	0	6	6	ო	4	ഹ
	Query Match Length	260	253	253	253	242	286	251	247	524	524	247	524	524	524	524	281	524	524	524	524	274	274	274
. d	Query	98.8	81.2	81.2	81.2	72.4	70.4	70.3	70.0	68.1	68.1	68.1	67.9	67.9	67.8	67.8	67.2	67.1	67.1	66.8	8.99	66.5	66.5	66.5
	Score	1381	1135	1135	1135	1011.5	983.5	982.5	978.5	952.5	952.5	952	949.5	949.5	947.5	947.5	939	937.5	937.5	933.5	933.5	929.5	929.5	929.5
	Result No.	г	7	m	4	S	9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

WPI; 2005-664872/68. N-PSDB; AEC92006.

Abg97808 Mouse MAB	Abg35311 Thrombopo	Aab23819 Plasmid p	Aag67495 Amino aci	Aam47633 Murine MA	Abg97810 Mouse MAB	Abg35313 Thrombopo	Adr43335 B7.1-scFv	Adr43337 Anti-NKG2	Aea06285 Anti-CD47	Abp45980 Human BLy	Adg96807 Single ch		Aef26295 Humanized	Aab23818 Plasmid p	Aag67494 Amino aci	Aam47632 Murine MA	Abg97809 Mouse MAB			Aea06284 Anti-CD47	Aab23820 Plasmid p
ABG97808	ABG35311	AAB23819	AAG67495	AAM47633	ABG97810	ABG35313	ADR43335	ADR43337	AEA06285	ABP45980	ADG96807	AED78860	AEF26295	AAB23818	AAG67494	AAM47632	ABG97809	ABG35312	AEA06282	AEA06284	AAB23820
4 .	4	4 3	4	4 5	4	4 5	7 8	8	5	4	4 7	9	6 0	1 3	1 4	1 5	1	1	9	6	1 3
27	27	27	27	27	27	274	69	70	20	24	24	24	24	27	27	27	27	27	25	20	27
66.5	66.5	66.4	66.4	66.4	66.4	66.4	66.3	66.3	66.3	66.1	66.1	66.1	66.1	62.9	62.9	62.9	62.9	62.9	65.9	62.9	65.8
929.5	929.5	928.5	928.5	928.5	928.5	928.5	927.5	927.5	927	924.5	924.5	924.5	923.5	921.5	921.5	921.5	921.5	921.5	921	921	920.5
24	25	56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	4

ALIGNMENTS

cytostatic; immunostimulant; pharmaceutical; protein interaction; therapeutic; immune modulation; solid tumor; leukemia; colorectal tumor; breast tumor; uterine cervix tumor; uterine civicoids; ovary tumor; gynecology and obstetrics; polycystic ovary syndrome; antiinfertility; gynecology; growth disorder; prostate tumor; prostate disease; andrology; genitourinary disease; pituitary tumor; endocrine disease; andrology; genitourinary disease; pituitary tumor; endocrine disease; multiple myeloma; menatological disease; immune disorder; central nervous system tumor; neurological disease; glioma; astroblastoma; neoplasm; single chain antibody; BC-12. Single chain variable fragment antibody BC-12 protein SEQ ID NO 2. Saven A; .2 /note= "Encoded by ATG" /note= "Encoded by GCA" Location/Qualifiers AEC92007 standard; protein; 260 AA. Janda KD, 13-FEB-2004; 2004US-0544807P. 10-NOV-2004; 2004US-0626726P. 11-FEB-2005; 2005US-00056825. 14-FEB-2005; 2005WO-US004612. 01-DEC-2005 (first entry) (SCRI) SCRIPPS RES INST. Felding-Habermann B, Key Misc-difference Misc-difference WO2005091805-A2 Homo sapiens. 06-OCT-2005. Synthetic AEC92007; RESULT 1 AEC92007 N

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The invention describes an antibody comprising a ligand mimetic, which differentially binds to an activated alphavbeta 3 integrin receptor differentially produced on a cell in a merestatic state compared to a similar, non-metastatic cell, and does not bind to a non-activated alphavbeta 3 integrin receptor. Also described are: a pharmaceutical composition comprising the antibody; treating a disease state in a mammal; a cell line comprising a tumor cell variant with a metastatic homing propensity to a target tissue; producing an antibody phage population amammal by treatment with a cancer therapeutic; inducing or enhancing an immune response to an antigen in a mammal detecting tumor cell surface in a mammal by treatment with a cancer therapeutic; inducing or enhancing an immune response to an antigen in a mammal by treatment with cells liable to undergo metastasis associated with a disease state; an isolated Bc-12 or Bc-15 control of a second tidentifying cells liable to undergo metastasis associated with a disease state; an isolated Bc-12 or Bc-15 polymucleotide comprising a nucleotide sequence that has at least 90% percent identity to a fully defined 802 or 752 bp sequence (SEQ ID NO. 1 or 3) given in the specification; an isolated polypeptide comprising a nucleotide sequence that has at least 90% comprising the polymucleotide in which the nucleotide sequence identity to SEQ ID NO. 1 or 3, or shares a biological function with Bc-12 or Bc-15; a vector comprising the polymucleotide in which the nucleotide sequence of the polymucleotide in a host cell; a host cell comprising the polymucleotide in a respect of the cell; and comprising the polymucleotide in a host cell; and expression vector comprising the polymucleotide or progeny of the cell; and expression in expression of the polymucleotide or progeny of the cell; and expression cell the polymucleotide in a host cell; and expression in expression of treating neoplastic disease, solid tumor, hematological malignancy, treating neoplastic disease, solid tumor, hema
      specifically binds to activated alphavbeta3 integrin receptor, useful for treating, e.g. neoplastic disease, solid tumor, leukemia, or benign or malignant breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polycystic ovary syndrome, endometrial polyps, prostate cancer, prostatic hypertrophy, pituitary cancer, adenomyosis, adenocarcinomas, meningioma, melanoma, bone cancer, multiple myeloma, CNS cancer, glioma, or astroblastoma. This is the amino acid sequence of single chain variable fragment antibody BC-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer, uterine leiomyomas, ovarian cancer, endometrial cancer,
                                                                                                                                                                                Claim 2; SEQ ID NO 2; 109pp; English
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Sequence 260 AA;

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                                                                                                                                                                                                                                                                                                                 SPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQG 240
                                                                                                                                                         61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSSGG 120
                                                                                                                                                                               62 YQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSSGG 121
                                                                                                                                                                                                                                     GGSGGGGGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQ 180
                                                                                                                                                                                                                                                           GGSGGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQ 181
                                                                                                                                                                                                                                                                                                                                       SPRRIIYKVSNRDSGVPDRFSGSGGTDFTLKISRVBAEDIGVYYCMQGTHWPPRTFGQG 241
                                                                               1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWINNGNTHY 60
                                                                                                                   61
                                                                                                                   2 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWINNGNTHY
                                         Gaps
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   Length 260;
                                         1; Indels
Score 1381; DB 9;
Pred. No. 3.2e-91;
0; Mismatches 1;
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98.8%;
99.6%;
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                     Best Local Similarity 99.6
Matches 258; Conservative
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ABP45953 standard; protein; 253 AA

ABP45953 ID ABP4 RESULT 2

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLVS) polypeptides. BLVS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLVS. The antibodies bind to BLVS and so may be used to detect and quantitate the presence of BLVS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLVS. They may also be administered to treat diseases associated with aberrant BLVS expression and activity such as cancer, immune, and autoimmune disorders and addiseases, e.g. systemic lupus errythematosus, rheumatoid architis, immunodeficiency (e.g. common variable immunodeficiency (VID) and
                                                                                                                                   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; fimunosuppressive; immunostimulativ; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 VSSGGGGGGGGGGGGGG--EIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQKPQGRVTMTTDTSTSTAYMBLRSLRSDDTAVYYCARDPRGDDE-----PYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OVOLOQSGAEVKEPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilbert D;
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tive 15; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2744-2745; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                 Human BLyS binding scFv SEQ ID 1964.
                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2001; 2001WO-US019110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-0277379P
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                           19-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-114799/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                          WO200202641-A1.
                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-2000;
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Gaps

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10; DB 7;

Length 253; Indels 173

233 239

115 120

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61 AQKLQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCARNPYYYDSSEGFFDYWGQGTMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VSSGGGGGGGGGGGGGARDDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW
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                                                                                                                                                                                                                                           1 QVQLQQSGAEVKEPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                            116 VSSGGGGSGGGGGGGS--EIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSW
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                                                                                                                                                                                                                                                                                                                           61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDE-----PYWGQGTLVT
                                                                                                                                                                                                             3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNTHY
                                                                                         81.2%; Score 1135; DB 7;
86.2%; Pred. No. 1.4e-73;
iive 15; Mismatches 10
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2001US-00880748.
2001US-031469P.
2001US-0340817P.
2002US-0293418.
2004US-0543296P.
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2001US-0276248P.
2001US-0277379P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFTFGOGTKMEIKR 253
                                                                                      Query Match
Best Local Similarity 86.2%
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-2006 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RUBEN S M.
                                      Sequence 253 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS2005255532-A1.
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15-JUN-2001;
16-NOV-2001;
19-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-2000;
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21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-2002;
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(CHOI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to Chromosome 1343 and encodes a protein that is a member of the tumour chromosome 1343 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (GCFWs) derived, preferably, from the variable compart thereof, of either human, murine, rat or monkey BLyS. The fragment thereof, of either human, murine, rat or monkey BLyS. The creep invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This attinflammatory, antiasthmatic, antiallergic and cytostatic. This cinvention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format of directely from WIPO at ftp.wipo.int/published otc_sequences.
181 FQQRPGQSPRKLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQATRW- 239
                                                                                            FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stimulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel antibody that immunospecifically binds to a B lymphocyte stimu (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody, B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain antibody that immunospecifically binds BLyS SeqID 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaughan TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 1964; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            ADG96780 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-2002; 2002WO-US036496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                             PRTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-505530/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-2003.
                                                                                                                                                                                                          234
                                                                                                                                                                                                                                                                   240
                                   121
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Antiarthritic, Neuroprotective, Muscular-Gen.; Antiasthmatic;
Antiallergic; Antimicrobial; Anti-HIV; Cytostatic; B-lymphocyte;
antibody; autoimmune disease; b-cell lymphoma;
systemic lupus erythematosus; rheumatoid arthritis; immune disorder;
                                                             Antiinflammatory; Dermatological; Immunosuppressive; Antirheumatic;
                                           Human B Lymphocyte binding scFv fragment protein, SEQ ID 1964.
                                                                                                                                                                                                                                                                                                                                                             Hilbert D;
                                                                                                       inflammation; infectious disease; hyperproliferation.
                                                                                                                                                                                                                                                                                                                                                             Vaughan T,
                                                                                                                                                                                                                                                                                                                                                             Choi GH,
                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                BARASH S C CHOI G H. VAUGHAN T. HILBERT D.
                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                                                                                                                                  (VAUG/)
(HILB/)
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The invention relates to a novel antibody that immunospecifically binds to a B Lymphocyte Stimulator protein. The protein comprises an amino acid sequence that is 85% identical to the VH domain of any one of the singlechain variable fragments (scrys) of SEQ ID NOS. 1-2128, and/or an amino acid sequence that is at least 85% identical to the VL domain of any one of the scrys of SEQ ID NOS. 1-2128. The invention further comprises: an isolated nucleic acid molecule encoding the antibody; an isolated cell ine that expresses the antibody; a method for detecting the expression of a B Lymphocyte Stimulator protein; a method for diagnosing an cutoimmune disease or a B cell cancer; and a method for treating, preventing, or ameliorating an autoimmune disease or a B cell cancer. The autoimmune disease or a B cell cancer. The autoimmune disease or a B cell cancer. The autoimmune disease or a B cell cancer. The autoimmune disease or a B cell cancer. The autoimmune disease is systemic lupus erythematosus or rheumatoid arthritis. It can also be used for diagnosing, treating, and preventing immune disease (e.g. multiple collaboration of alsoness, myssthenia argaryis, or Hashimoto's disease) inflammatory, and alsoness or allowing and preventing immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders (e.g. asthma or allergic disorders), infectious diseases (e.g. AIDS), and proliferative disorders (e.g. leukemia, carcinoma, or AIDS), and proliferative disorders (e.g. leukemia, carcinoma, or polymphoma). This sequence represents a single-chain variable fragment polypeptide that immunospecifically binds to a B Lymphocyte Stimulator protein of the invention. Note: This sequence is not shown in the specification. It has been electronically downloaded from the USPTO
                                                             New antibodies that immunospecifically binds to B Lymphocyte Stimulator protein, useful for diagnosing, treating, or preventing autoimmune disease, e.g. systemic lupus erythematosus or rheumatoid arthritis, or E
                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1964; 240pp; English.
   WPI; 2005-808635/82.
                                                                                                                                                           cell cancer
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Sequence 253 AA;

4 FQQRPGQSPRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQATRW- 239 61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDE-----PYWGQGTLVT 115 VSSGGGGGGGGGGGGGS--EIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSW 173 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWP 233 9 3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNTHY QVQLQQSGAEVKEPGASVKVSCKASGYTPTSYGISWVRQAPGQGLEWMGWISAYNGNTNY Gaps 10; 81.2%; Score 1135; DB 9; Length 253; 86.2%; Pred. No. 1.4e-73; 10; Indels 15; Mismatches PRTFGQGTKVEIKR 247 Matches 219; Conservative Local Similarity 240 116 121 174 181 234 Query Match 셤 8 ઠ δ 셤 ð ð

Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody; diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy; BIOC7. Amino acid sequence of antibody BIOC7. AAY21884 standard; protein; 242 AA (first entry) 24-SEP-1999 AAY21884; AAY21884 RESULT * A K K B K B K K K K B

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prostate-specific antigen (PSA) and anti-chymotrypein (ACT), and has an affinity for the complex which is at least 10 fold higher than the affinity for either PSA or ACT alone. The antibody is used in diagnostic assays to detect PSA-ACT in serum samples from patients. The levels of PSA-ACT complex increase in patients suffering from prostate cancer compared to the levels in patients with benign or no growths in the prostate. Therefore detection of PSA in complex with ACT is useful for the early detection of prostate tumours, by distinguishing between benign of mailgnant conditions of the prostate as well as for the management of patients with prostate cancer, such as the disclosure of metastasis and the monitoring of the PSA levels after treatment. The antibodies may also burification of PSA-ACT unlike prior art antibodies which bind to PSA-ACT alone. Diagnostic assays using the antibodies are 1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTPSNYGITWVRQAPGQGLEWMGWIN--NGNT 1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNT 59 HYAQKEQCRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSS examples of antibodies directed against PSA-ACT. The present sequence represents the amino acid sequence of antibody BIOC7 Gaps more accurate in diagnosing prostate cancer as they only detect the intact complex of PSA-ACT. Sequences AAV21880-884 represent specific The invention relates to an antibody that binds a complex between New anti-complex antibody useful for diagnosing prostate cancer. 9. DB 2; Length 242; 72.4%; Score 1011.5; DB 2; Length 78.7%; Pred. No. 1e-64; Live 20; Mismatches 24; Indels /label= unknown /note= "encoded by TST" 'note= "encoded by TCN" Claim 29; Page 28-30; 42pp; English. Location/Qualifiers /label= unknown /note= "encoded by (BOEF) BOEHRINGER MANNHEIM CORP. 'label= unknown 98EP-00122546 97US-0067428P Query Match Best Local Similarity 78.7% Matches 196; Conservative Mahoney W, WPI; 1999-432068/37. N-PSDB; AAX86942 Sequence 242 AA; Misc-difference Misc-difference Misc-difference 01-DEC-1998; 03-DEC-1997; Homo sapiens 11-AUG-1999 EP934953-A2 Winter GP, ð d ઠે

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AAB70171 standard; protein; 251
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                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                   Recombinant antibody #1
                                                                                                                                                                                                                                                                                                                                                                                                           Norton EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-182730/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel antibody sequences, which acts against lesioned tissue. Also claimed is a method (M1) for isolating polynucleotide encoding the antibodies, which involves (a) isolating B cells that is infiltrated into lesioned tissue, and (b) acquiring polynucleotide that encodes an antibody from the isolated B cells. The antibodies are useful for treating cancer lesions, arteriosclerosis, inflammatory disease or autoimmune disease. The present sequence was used
107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 WGQGTLVTVSSGGGGGGGGGGGGGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolating polynucleotide that encodes antibody which acts against lesioned tissue, involves isolating B cells that is infiltrated into lesioned tissue, and acquiring polynucleotide that encodes antibody from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive; human; antibody; cancer lesion; arteriosclerosis; inflammatory disease; autoimmune disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                         Tsunoda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR------DPRGDDEPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WGQGTLVTVSSGGGGGGGGGGGGGBIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEMMGWINPNSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYG1TWVRQAPGQGLEWMGW1 -- NNGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYAQKFQGRVTMTRDTSISTAYMBLSRLRSDDTAVYYCARGYDILTGYGWFDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                       Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                            Human antibody related protein sequence, SEQ ID 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%; Score 983.5; DB 8;
llarity 72.0%; Pred. No. 1.2e-62;
Conservative 21; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                      Pujii E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 184; 200pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                      Yoshida K,
                                                                                                                     ADP03811 standard; protein; 286 AA
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RES PTE LTD.
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                                                                                                                                                                                                                                                                                                                                                             22-NOV-2002; 2002JP-00339241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to illustrate the invention.
                                                                                                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                    (CHUS ) CHUGAI SEIYAKU (PHAR-) PHARMALOGICALS
                                    239 QGTKVEIKR 247
                                                          234 QGTKVEIKR 242
                                                                                                                                                                                                                                                                                                                                                                                                                       Tsuchiya M, Suzuki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-450382/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 198; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated B cells.
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                                                                                                                                                                                                                                                                                       WO2004048571-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 286 AA;
                                                                                                                                                                    26-AUG-2004
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                                                                                                                                             ADP03811;
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Matches
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                               196 NKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDPTLTISTLQAEDVAVYYC 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specifically binding to sperm agglutination antigen-1 (SAGA-1). The recombinant antibody has two peptide fragments of the S19 antibody and the fragments are joined together by a linker. The recombinant monoclonal antibodies are useful in a passive immunity composition for contraception as they inhibit the ability of sperm to fertilize an egg. The antibodies may be used e.g. as an active ingredient of a spermistatic agent, or as a component of a spermicidal contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant antibody derivative of monoclonal antibody S19, useful a reagent for purifying or detecting human spermatozoa, as an active ingredient of a spermistatic agent, or as a component of a spermicidal
168 N-TYLSWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI --NNGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                              227 MOGTHWPPRIFGOGIKVEIKRGLGGLVDYKDDDDK 261
                                                                                                                                                                            Antibody; sperm; S19; contraception.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Page 41-42; 48pp; English
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diabetes and tumors, comprises using peptides that bind to insulin or insulin-like growth factor receptors. Pillutla R, Brandt J; Ostergaard S, Mandecki WS;

The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor (IGF-1) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. AAU88034-AAU99957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the invention

Sequence 247 AA;

Query Match

3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI----NNGNT 58 2 70.0%; Score 978.5; DB 5; Length 247; 74.2%; Pred. No. 2.4e-62; ive 28; Mismatches 31; Indels 5; Best Local Similarity /7... Matches 184; Conservative Similarity

180 238 181 GOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVBAEDVGVYYCMQGTHW-PYTFG 59 HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSS 179 GOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFG 119 GGGGGGGGGGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRP 239 QGTKVEIK 246 240 QGTKLEIK 247 RESULT 9 8 ద ઠે ద 셤 ሯ g

Anti-TPO single chain antibody hVB22B q-wz5. AEA44228 standard; protein; 524 AA 25-AUG-2005 AEA44228;

AEA44228

hemostatic; single chain antibody; protein purification; antibody engineering; antibody production; thrombocytopenia; hemostatic; hematological disease; hVB22B q-wz5.

WO2005056604-A1. 23-JUN-2005 10-DEC-2004; 2004WO-JP018506.

12-DEC-2003; 2003JP-00415746. 12-MAR-2004; 2004JP-00071763. 27-AUG-2004; 2004JP-00248323.

(CHUS) CHUGAI SEIYAKU KK.

Tsuchiya M, Orita T, Nakano K, Isunoda H,

WPI; 2005-445149/45. N-PSDB; AEA44227 variants like Anti-Mpl antibodies including antihuman Mpl antibody and variants l genetically-engineered antihuman Mpl diabody, applicable in drug compositions for use in chemotherapy of thrombocytopenia and other diseases associated with Mpl mutation.

Claim 29; SEQ ID NO 293; 106pp; Japanese.

The invention describes an antibody is a single-chain polypeptide with TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2 TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2 CE heavy-chain variable regions and 2 light-chain variable regions. Also described are: a chimeric antibody for binding with human Mpl; an antibody for binding with human Mpl and monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies with binding activity for soluble Mpl; antibodies containing a heavy-chain variable region with CDR (complementary-determinant regions 1, 2 and 3); antibodies containing heavy and light-chain variable regions with CDR 1, and 3 selected from the already specified groups in 18 combinations; antibodies containing a heavy-chain variable region with RR1, 2, 3 and 4; antibodies containing a light-chain variable region with RR1, 2, 3 and 4; epitope-recognizing antibodies the antibodies with the heavy and light-chain variable region RR1, 2, 3 and 4; epitope-recognizing antibodies the antibodies with the heavy and light-chain variable regions and amino acid sequences;

Matsumoto Y;

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have equivalent activity as such antibodies; vectors containing these polynucleotides; host cells carrying such polynucleotides or vectors; and drug compositions containing these antibodies. The antibodies are applicable in drug compositions for use in chemotherapy of thrombocytopenia and other diseases associated with Mp1 mutation such as congenital amegakaryocytic thrombocytopenia. These antibodies can include antihuman Mp1 antibody and variants like genetically-engineered antihuman Mp1 diabody and (humanized) antihuman Mp1 sc(Fv)2. Such antibodies are soluble to enhance binding ability. The diabody and sc(Fv)2 show high agoinstic activity against antihuman Mp1 antibody, such activity of which is comparable or superior to that of the natural ligand, human TPO. This is the amino acid sequence of a single chain antibody human FPO. This
antibodies that can recognize the an amino acid moiety in human Mpl from positions 26-271, polymucleotides encoding these antibodies; polymucleotides hybridizable with the polymucleotides that encode the antibodies under stringent conditions and the antibodies encoded by which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 YAQKPQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDE---PYWGQGTLVTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 YNGKFRVRVTITADESTSTAYMELSSLRSEDTAVYYCA---RGYDDYSFAYWGQGTTVTV 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody; myeloproliferative leukemia virus oncogene; Mpl; antibody engineering; humanized antibody; platelet; thrombocytopenia; hemostatic; hematological disease; ds; coding sequence; single chain antibody.
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                                                                                                                                                                                                                                                                                                                                                                       68.1%; Score 952.5; DB 9; Length 524; 74.8%; Pred. No. 3.8e-60; ive 25; Mismatches 30; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                               Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   Sequence 524 AA;
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The invention relates to remedies for thrombocytopenia comprising an sc(Fv)2 (a double single chain antibody comprising 2 heavy chains and 2 light chains, often referred to as a diabody) with binding activity coward TPO (thrombopoietin) receptor (Mpl, myeloproliferative leukemia virus oncogene) as active ingredient. The antibodies comprise human framework regions (FR) grafted to mouse complementarity region (CDR).

Also included are remedies for thrombocytopenia containing antibodies (thrombocytopenia containing antibodies for thrombocytopenia containing antibodies (which have a heavy-chain variable region with CDR1, CDR2 and CDR3 that have amino acid sequences of AEBC02043-AEBC02045, respectively, and/or a light-chain variable region with CDR1, CDR2 and CDR3 that have amino acid sequences of AEBC02044-AEBC02046, respectively, and/or a light-chain and/or insertion of some amino acids), remedies for thrombocytopenia containing antibodies that can recognize amino acid sites of human Mpl and/or insertion of some amino acids), remedies for thrombocytopenia containing antibodies that can recognize amino acid sites of human Mpl cremedies. The remedies are for the treatment of thrombocytopenia containing antibodies are for the treatment of thrombocytopenia continity against antihuman Mpl antibody, and the activity is comparable or superior to that of human TPO (thrombopoietin) which is a natural cativity against antihuman Mpl antibody, and the activity is comparable or superior to that of human TPO (thrombopoietin) which is a natural cativity against antihuman Mpl antibody, and the activity is comparable or superior to that of human TPO (thrombopoietin) which is a natural can extremely effective because they have high against antihuman Mpl antibody, and the activity and antibody (or superior that of human TPO (thrombopoietin) which is a natural cativity against antihuman mpl (thrombopoietin) antibody (or diabody) derived from the mouse anti-Mpl antibody et printed from the mouse anti-Mpl antibody et printed from the m
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                                                                                                                 Remedies for thrombopenia as well as agents for increasing number of platelets comprises e.g. Mpl-recognizing antibodies with high agonistic activity against antihuman Mpl antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                       Example 3; SEQ ID NO 101; 71pp; Japanese
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Matches 190; Conservative
Tsuchiya M, Orita T,
                                                                      N-PSDB; AEE02145
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N-PSDB; AEC92008

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(first entry)
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Single chain variable fragment antibody BC-15 protein SEQ ID NO 4.

cytostatic; immunostimulant; pharmaceutical; protein interaction; therapeutic; immune modulation; solid tumor; leukemia; colorectal tumor; breast tumor; uterine cervix tumor; uterine cervix tumor; uterine cervix tumor; uterine cervix spracologisal; polyp; growth disorder; ovary syndrome; antiinfertility; gynecological; polyp; growth disorder; prostate tumor; prostate disease; andrology; genitourinary disease; pituitary tumor; endocrine disease; andrology; genitourinary disease; pituitary tumor; endocrine disease; multiple myeloma; melanoma; bone tumor; musculoskeletal disease; entriple myeloma; hematological disease; immune disorder; central nervous system tumor; neurological disease; glioma; astroblastoma; neoplasm; single chain antibody; BC-15.

Homo sapiens

Synthetic

/note= "Encoded by GATGACAAATAA" Location/Qualifiers Misc-difference

WO2005091805-A2

06-OCT-2005.

14-FEB-2005; 2005WO-US004612.

13-FEB-2004; 2004US-0544807P. 10-NOV-2004; 2004US-0626726P. 11-FEB-2005; 2005US-00056825.

(SCRI) SCRIPPS RES INST.

Saven Janda KD, Pelding-Habermann B,

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WPI; 2005-664872/68.

New scFv Bc-12 or Bc-15 antibody comprises ligand mimetic, which specifically binds to activated alphavbeta3 integrin receptor, useful for treating, e.g. neoplastic disease, solid tumor, leukemia, or benign or malignant breast cancer.

Claim 3; SEQ ID NO 4; 109pp; English

The invention describes an antibody comprising a ligand mimetic, which specifically binds to an activated alphavheta 3 integrin receptor differentially produced on a cell in a metastatic state compared to a similar, non-metastatic cell, and does not bind to a non-activated alphavheta 3 integrin receptor. Also described are: a pharmaccutical composition comprising the antibody; treating a disease state in a mammal composition comprising a tumor cell variant with a metastatic homing propensity to a target tissue; producing an antibody phage population having affinity for a tumor cell target; detecting uncor cells in a mammal by treatment with a cancer therapeutic; inducing or enhancing an maning a matigen in a mammal; detecting or enhancing an expense to an antigen in a mammal; detecting or enhancing an surface receptor on a metastatic tumor cell surface in a mammalian tissue surface receptor on a metastatic tumor cell surface in a mammalian tissue sample; interfering with cells liable to undergo metastasis associated with a disease state; identifying cells liable to undergo metastasis associated with a disease state; an isolated Bc-12 or Bc-15 polymucleotide comprising a nucleotide sequence that has at least 90% percent identity to a fully defined 802 or 752 bp sequence (SEQ ID NO. 1 or 3) or shares a biological function with Bc-12 or Bc-15; a vector comprising the polymucleotide in which the nucleotide sequence of the polymucleotide in which the nucleotide sequence that comprising the polymucleotide in which the mucleotide sequence of the polymucleotide in which the mucleotide sequence of the polymucleotide in which he mucleotide sequence of the polymucleotide in which he mucleotide sequence of the polymucleotide in which he mucleotide sequence of the polymucleotide in which he mucleotide sequence of the polymucleotide in which he mucleotide sequence of the polymucleotide or progeny of the cell; and determining anti-metastic cativity of a test compound in a mammal. The antibody is useful for comprising the cell The invention describes an antibody comprising a ligand mimetic, which

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cancer, uterine leiomyomas, ovarian cancer, endometrial cancer, prostatic polycystic ovary syndrome, endometrial polyps, prostate cancer, prostatic hypertrophy, pituitary cancer, adenomyosis, adenocarcinomas, meningioma, melanoma, bone cancer, multiple myeloma, CNS cancer, glioma, or astroblastoma. This is the amino acid sequence of single chain variable
                                                                                                                                                                                                                                                                                                                                    118
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antibody engineering; antibody production; thrombocytopenia; hemostatic;
hematological disease; hVB22B u2-wz5.
   cancer, uterine
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genetically-engineered antihuman Mpl diabody, applicable in drug
compositions for use in chemotherapy of thrombocytopenia and other
diseases associated with Mpl mutation.
                                                                                                                                                                                                                         Indels 18;
                                                                                                                                                                                    Length 247;
colorectal cancer, benign or malignant breast
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                                                                                                                                                                                    Query Match 68.1%; Score 952; DB 9; L
Best Local Similarity 71.8%; Pred. No. 1.9e-60;
Matches 188; Conservative 29; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-TPO single chain antibody hVB22B u2-wz5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOGTKVDIKRGLGGLVDYKDDD 247
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12-MAR-2004; 2004JP-00071763.
27-AUG-2004; 2004JP-00248323.
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                                                                                                           fragment antibody BC-15.
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N-PSDB; AEA44221.
                                                                                                                                                   Sequence 247 AA;
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The invention describes an antibody is a single-chain polypeptide with TPO (thrombopoietin) receptor (Mpl) binding activity that contains the 2 TPO (thrombopoietin) receptor (Mpl) binding activity that contains the 2 Deavy-Chain variable regions and 2 light-chain variable regions. Also described are: a chimeric antibody for binding with Mpl; an antibody for binding with Mpl; an antibody for binding with Mpl; an antibody for binding with human Mpl and monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies with binding activity for soluble Mpl; antibodies with binding activity for soluble Mpl; antibodies with Dinding activity for soluble Mpl; antibodies containing heavy and light-chain variable regions with CDR 12 and 3; antibodies containing a leavy-chain variable regions with CDR 12 and 3; antibodies containing a heavy-chain variable regions with CDR 12, and 4; antibodies containing a heavy-chain variable regions with RPI; 2, 3 and 4; antibodies containing a neavy-chain variable regions with RPI; 2, 3 and 4; antibodies that can recognize the antibodies with the heavy and light-chain variable regions and amino acid sequences; antibodies that can recognize the an amino acid sequences; antibodies under stringent conditions and the antibodies; polymucleotides hybridizable with the polymucleotides encoded by which have equivalent activity as such antibodies; and polymucleotides host such antibodies; vectors containing these polymucleotides in the antibodies; and polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides on the polymucleotides o
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Claim 29; SEQ ID NO 287; 106pp; Japanese.
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79 YNGKFRVRVIITADESTSTAYAMQLSSLRSEDTAVYYCA---RGYDDYSFAYWGQGTTVTV 135 117 SSGGGGSGGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQ 176 136 SSGGGGGGGGGGGGGDIVMTQSPLSLPVTPGEPASISCRSSKSLLHSNGNTYLYWFLQ 195 2 AQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNTH 60 YAQKFQGRVTMTTDTSTSTAYMBLRSLRSDDTAVYYCARDPRGDDE---PYWGQGTLVTV 6 67.9%; Score 949.5; DB 9; Length 524; 74.4%; Pred. No. 6.2e-60; ive 26; Mismatches 30; Indels 9; Query Match. 67.9 Best Local Similarity 74.4 Matches 189; Conservative ద ઠે g g

Sequence 524 AA;

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177 RPGQSPRRLIYKVSNRDSGVPDRFSGSGGTDFTLKISRVEAEDIGVYYCMQGTHWPPRT 236

AEE02142 standard; protein; 524 AA (first entry) 26-JAN-2006 AEE02142; RESULT 13 AEE02142

Anti-Mpl sc(Fv)2 antibody hVB22B u2-wz4.

Antibody; myeloproliferative leukemia virus oncogene; Mpl;

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The invention relates to remedies for thrombocytopenia comprising an sc(Fv)2 (a double single chain antibody comprising 2 heavy chains and 2 c(Fv)2 (a double single chain antibody comprising 2 heavy chains and 2 tight chains, often referred to as a diabody) with binding activity y coward TPO (thrombopoietin) receptor (MpJ, myeloproliferative leukemia virus oncogene) as active ingredient. The antibodies comprise human cortaining antibodies (comprise nortaining antibodies comprise human containing antibodies (which have a last can bind with human Mpl and monkey Mpl, remedies for thrombocytopenia containing antibodies (which have a complements of the carbot region with CDR1, CDR2 and CDR3 that have amino acid sequences of ABE02043-AEE02045, respectively, and/or a light-chain cortaining antibodies (which have a managed or a NEE02046-AEE02048, or antibodies having amino acid sequences of AEE02048 for modification by substitution, deletion, addition and/or insertion of some amino acids, remedies for thrombocytopenia containing antibodies that can recognize amino acid sites of human Mpl from positions 126-274, and agents for increasing platelets containing containing antibodies are for the treatment of thrombocytopenia cortaining are extremely effective because they have high agonistic artibodies are extremely effective because they have high agonistic activity against antihuman Mpl antibody, and the activity is a natural cortaining the present sequence represents a humanized single chain antibody cortained from the mouse anti-Mpl antibody (WB22B). Note: The sequence data for this patent did not form part of remedies cortained in electron format directly form WPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remedies for thrombopenia as well as agents for increasing number of platelets comprises e.g. Mpl-recognizing antibodies with high agonistic activity against antihuman Mpl antibody.
antibody engineering; humanized antibody; platelet; thrombocytopenia; hemostatic; hematological disease; ds; coding sequence; single chain antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 100; 71pp; Japanese
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                                                                                                                                                                                                                                                                                                                 11-MAY-2004; 2004JP-00141618.
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                                                                                                                                                                                                                                                                                                                                                                                                       Isuchiya M, Orita T,
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                                                                                                                                                                                  WO2005107784-A1.
                                                                                               Homo sapiens
                                                                                                                     musculus.
                                                                                                                                                                                                                             17-NOV-2005.
                                                                                                                                          Synthetic.
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17 SSGGGGGGGGGGGGGGGTULTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQ 176 2 AQVQLVQSGABVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI - - NNGNTH 19 SQVQLVQSGPEVKKPGASVKVSCKASGYTPTNSWMNWVRQRPGKGLEWIGRIYPGDGETI 60 YAQKEQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDE---PYWGQGTLVTV ., 67.9%; Score 949.5; DB 9; Length 524; 74.4%; Pred. No. 6.2e-60; 30; Indels 26; Mismatches 74.48; Matches 189; Conservative Query Match Best Local Similarity Sequence 524 AA; 셤 ò ઠે 셤 ò

specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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The invention describes an antibody is a single-chain polypeptide with TPO (thrombopoietin) receptor (Mp1)-binding activity that contains the 2 meavy-chain variable regions and 2 light-chain variable regions. Also described are: a chimeric antibody for binding with Mp1; an antibody for binding with Mp1; an antibody for binding with human Mp1 and concise with squistic activity for soluble Mp1; antibodies with binding activity for soluble Mp1; antibodies containing a heavy-chain variable regions with CDR 12 and 3); antibodies containing a light-chain variable region with CDR 12 and 3); antibodies containing a light-chain variable region with CDR 12 and 3); antibodies containing a light-chain variable region with CDR 12 and 3; antibodies containing a light-chain variable region with CDR 12 and 4; antibodies containing a light-chain variable region with CDR 12. and 4; antibodies containing a light-chain variable region with RPI, 2; 3 and 4; antibodies containing a light-chain variable region with CDR 12. antibodies that can recognize the antibodies with the heavy and light-chain variable regions and amino acid sequences; antibodies that can recognize the amino acid molety in human Mp1 from positions 26-274; polymucleotides encoding these antibodies encoded by which cantibodies under stringent conditions and the antibodies encoded by which have equivalent activity as such antibodies; vectors containing these
                      SSGGGGGGGGGGGGSDIVMTQSPLSLPVTPGEPASISCRSSKSLLHSNGNTYLYWFLQ 195
                                                           RPGQSPRRLIYKVSNRDSGVPDRFSGSGGTDFTLKISRVEAEDIGVYYCMQGTHWPPRT 236
                                                                                   hemostatic; single chain antibody; protein purification;
antibody engineering; antibody production; thrombocytopenia; hemostatic;
hematological disease; hVB22B p-z.
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Hirata Y;
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                                                                                                                                                                                                                                                                                                                                                                                                 Anti-TPO single chain antibody hVB22B p-z.
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                                                                                                                                                                                                                                                                               AEA43937 standard; protein; 524 AA.
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27-AUG-2004; 2004JP-00248323.
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                                                                                                                                        FGQGTKVEIKRGLG 250
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N-PSDB; AEA43936.
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polynucleotides; host cells carrying such polynucleotides or vectors; and drug compositions containing these antibodies. The antibodies are applicable in drug compositions for use in chemotherapy of the applicable in the drug compositions are specially of the drug compositions are drug compositions and other diseases associated with Mp1 mutation such as congenital amegakaryocytic thrombocytopenia. These antibodies can include antihuman Mp1 antibody and variants like genetically-engineered antihuman Mp1 diabody and (humanized) antihuman Mp1 sc(FV)2. Such antibodies are soluble to enhance binding ability. The diabody and sc(FV)2 show high agonistic activity against antihuman Mp1 antibody, such activity of which is comparable or superior to that of the natural ligand, human TPO. This is the amino acid sequence of a single chain antibody hVB22B p-z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
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                                                                                                                                                                                                                                                                                                                                            19 SQVQLVQSGPEVKKPGASVKVSCKASGYTFTNSWMNWVRQRPGKGLEWMGRIYPGDGETI
                                                                                                                                                                                                                                                                                                                          2 AQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNTH
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                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                      DB 9; Length 524;
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                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                       31,
                                                                                                                                                                                                                                                    67.8%; Score 947.5; DB 9 74.8%; Pred. No. 8.6e-60;
                                                                                                                                                                                                                                                                                       24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 FGQGTKVEIKRGLG 250
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                                                                                                                                                                                                                                                                                     Matches 190; Conservative
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                                                                                                                                                                                                                   Sequence 524 AA;
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Synthetic.
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Remedies for thrombopenia as well as agents for increasing number of platelets comprises e.g. Mpl-recognizing antibodies with high agonistic activity against antihuman Mpl antibody.

Example 3; SEQ ID NO 61; 71pp; Japanese

The invention relates to remedies for thrombocytopenia comprising an sc(Fv)2 (a double single chain antibody comprising 2 heavy chains and 2 light chains, often referred to as a diabody) with binding activity toward TPO (thrombopoietin) receptor (Mpl, myeloproliferative leukemia virus oncogene) as active ingredient. The antibodies comprise human cramework regions (FR) grafted to mouse complementarity region (CDR). Also included are remedies for thrombocytopenia containing antibodies (chat can bind with human Mpl and monkey Mpl, remedies for thrombocytopenia containing antibodies (which have a heavy-chain variable region with CDR1, CDR2 and CDR3 that have amino acid sequences of AEB02043-AEB02045, respectively, and/or a light-chain variable region with CDR2 and CDR3 that have amino acid sequences of AEB02044 for antibodies having amino acid sequences of AEB02044 for antibodies having amino acid sequences of AEB02044 for antibodies having amino acid sequences of AEB02044 for modification by substitution, deletion, addition and/or insertion of some amino acids), remedies for thrombocytopenia containing antibodies that can recognize amino acid sites of human Mpl from positions 126-274, and agents for increasing platelets containing the active ingredients as already specified for the thrombocytopenia. Such antibodies are extremely effective because they have high agonistic activity against antihuman Mpl antibody, and the activity is comparable or superior to that of human TPO (thrombopoietin) which is a natural ligand. The presents sequence represents a humanized single chain antibody, and the activity defined from the mouse anti-and an (or diabody) derived from the mouse anti-Mpl antibody (VB22B). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 524 AA;

Gaps , 6 DB 9; Length 524; 31; Indels 67.8%; Score 947.5; DB 9 74.8%; Pred. No. 8.6e-60; Live 24; Mismatches 31 Best Local Simitarity '7...
Matches 190; Conservative Local Similarity Query Match Š

2 AQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNTH 59 SOVQLVQSGPEVKKPGASVKVSCKASGYTFTNSWMNWVRQRPGKGLEWMGRIYPGDGETI 78

> 셤 ò 셤 ò 셤 ઠે a ઠે 셤

177 RPGQSPRRLIYKVSNRDSGVPDRFSGSGGTDFTLKISRVEAEDIGVYYCMQGTHWPPRT 236

FGQGTKVEIKRGLG 250 237

Search completed: August 9, 2006, 13:09:33 Job time : 198 secs

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65.4%; Score 914.5;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 535 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38, Appl
Sequence 2, Appli
Sequence 30, Appli
Sequence 4, Appli
Sequence 53, Appl
Sequence 55, Appl
Sequence 113, App
Sequence 118, App
                                                                                         (without alignments)
456.910 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                         / BMC_Colerra_SiDS3/ptodata/2/iaa/5_COMB.pep:*
/ BMC_Colerra_SiDS3/ptodata/2/iaa/6_COMB.pep:*
/ BMC_Colerra_SiDS3/ptodata/2/iaa/7_COMB.pep:*
/ BMC_Colerra_SiDS3/ptodata/2/iaa/H_COMB.pep:*
/ BMC_Colerra_SiDS3/ptodata/2/iaa/pcTUS_COMB.pep:*
/ BMC_Colerra_SiDS3/ptodata/2/iaa/pcTUS_COMB.pep:*
/ BMC_Colerra_SiDS3/ptodata/2/iaa/RE_COMB.pep:*
/ BMC_Colerra_SiDS3/ptodata/2/iaa/RE_COMB.pep:*
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                                                                           9, 2006, 13:14:57; Search time 50 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-297-1181-2

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US-09-203-958A-4

US-08-875-811-53

US-08-875-811-53

US-09-491-788-113

US-09-490-707A-178

US-09-490-153-178

US-09-490-153-178

US-09-490-153-178

US-09-490-153-178

US-09-490-153-178

US-09-156-190

US-09-126-190

US-09-726-19A-190

US-08-331-398A-34

US-08-331-398A-34

US-08-331-398A-34

US-08-331-398-34

US-08-331-3978-34

US-08-331-3978-34

US-08-475-844-66

US-09-752-844-66

US-09-752-844-66

US-09-233-533-66

US-09-233-533-66

US-09-233-533-66

US-09-423-333-66

US-09-423-333-66
                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                     650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  using sw model
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                                                                                                                                                                                                                                                                                                                                                                 Patents AA:*
                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                             US-11-056-825-2
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Match Length

    protein search,

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                                                                           August
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881.5
870
866
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Maximum DB
                                                                                                                                                       Sequence:
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Perfect
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Sequence 4, Appli Sequence 38, Appli Sequence 7, Appli Sequence 5, Appli Sequence 63, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 90, Appli Sequence 90, Appli Sequence 14, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli Sequence 148, Appli	THERAPEUTICAL GARRETT &	#1.30
58.4 252 1 US-08-461-838-4 58.4 252 1 US-08-461-386-4 58.4 288 246 1 US-08-451-346-4 57.8 246 1 US-08-257-341-7 57.8 367 1 US-08-257-341-5 57.7 289 2 US-09-184-658-63 57.7 289 2 US-09-184-658-63 57.4 267 2 US-09-485-7378-2 56.8 711 2 US-09-485-7378-90 56.8 711 2 US-09-485-7378-85 56.7 541 2 US-09-485-7378-85 56.7 541 2 US-09-485-7378-85 56.7 541 2 US-09-485-7378-85 56.7 541 2 US-08-487-148-85 56.5 240 1 US-08-488-1138-148 56.5 240 1 US-08-646-360-148 56.5 240 2 US-08-338-148 56.5 240 2 US-08-338-148	ALIGNMENTS plication US/08983035A 464 MATION: T: CONSELLLER, EMMANUEL BRACCO, LAURENT INVENTION: B53 PROTEIN VARIANTS AND USES THEREOF F SEQUENCES: 59 NUENCE ADDRESS: RESSEE: FINNEGAN, HENDERSON, FARABOW, DUNNER, LLP DUNNER, LLP T: Washington TE: DC NTRY: USA 1: 2005-3315 1: 2006-3315	y disk ompatible PC-DoS/MS-DOS Release #1.0, Version A: US/O8/983,035A b: 1998 nknown> : PCT/FR96/01111 L-1996 : FR 95/08729 L-1995 LON: Iiam L. R: 47,114 WATTON:
228 816 229 816 310 808 313 802 313 807 314 802 315 794 317 794 410 790 441 790 444 790	SULT 1 -08-981-035A-38 -08-981-035A-38 Sequence 38, Applicat Patent No. 6326464 GENERAL INFORMATION APPLICANT: CONTES TITLE OF INVEN NUMBER OF SEQU CORRESPONDENCE ADDRESSEE ADTRESSEE STATE: 1; CITY: Wesl STATE: 0. COMPITE: 0.	CURRENT CORRENT COURRENT FILL FILL FILL RAP ATTORNE REG REG REG REG REG REG REG REG REG RE
	RESULT US-08- S-08- Pate:	

DB 2; Length 535;

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59 HYAOKFOGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGOGTLVTVSS 118
                                                                                                                                                                                                                                                             119 GGGSGGGGGGGSDVLMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRP 178
                                                                                                                                                                                                                                                                                                                                             179 GOSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKINRVEAEDLGVYYCWGGTH-SPLTFG 237
                                                                                                            9
                                                                                                                                                                           1 MAQVQLQESGABLVGSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDT
                                                                                                                                                                                                                                       GGGGGGGGGGGGGGTVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWPQQRP
                                                                                                                                                                                                                                                                                                                         GOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFG
                                                                     1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CONSEILLER, EMMANUEL
BRACCO, LAURENT
TITLE OF INVENTION: 153 PROTEIN VARIANTS AND THERAPEUTICAL
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,851A FILING DATE: 03-Oct-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142-01000
TELECOMMUNICATION: 102-408-4000
TELEPHONE: 202-408-4400
  Pred. No. 3.7e-67;
4: Mismatches 36;
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FILING DATE: 20-FEB-1998
APPLICATION NUMBER: PCT/FR96/01111
FILING DATE: 17-JUL-1996
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995
69.9%; Preα. αυ.
tive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-968-851A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Application US/09968851A Patent No. 6933373 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 I Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Strauss, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acida
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: DC
                         174; Conservative
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238 AGTKLELKR 246
                                                                                                                                                                                                                                                                                                                                                                                                          239 QGTKVEIKR 247
    Best Local Similarity
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GENERAL INCORNATION:
APPLICANT: Bracco, Laurent
APPLICANT: Bebussche, Laurent
APPLICANT: Debussche, Laurent
TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES
FILE REFERENCE: ST96030-US
CURRENT APPLICATION NUMBER: US/09/297,181
CURRENT PILING DATE: 1999-04-26
EARLIER APPLICATION NUMBER: PCT/FR97/01921
EARLIER FILING DATE: 1997-10-27
EARLIER FILING DATE: 1997-10-27
EARLIER FILING DATE: 1996-10-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                            118
                                                                                                                                                                                61 EYAPKEQGKATWTADTSSNTAYLQLSSLASEDTAVYYC--NFYGDALDYWGQGTTVTVSS 118
                                                                                                                                                                                                                                                              119 GGGGGGGGGGGGGSDVLMTQTPLTLSVTIGQPASISCKSSQSLLDSDGRTYLNWLLQRP 178
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                                                                                                                                                            59 HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSS
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                                                                              1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNT
                                         Gaps
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    Length 535;
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                                         Indels
65.4%; Score 914.5; DB 2;
69.9%; Pred. No. 3.7e-67;
ive 34; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.1%; Score 909.5; DB 2; 70.3%; Pred. No. 3.9e-67; ive 33; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-297-181-2; Sequence 2, Application US/09297181; Patent No. 6852509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.1%
Best Local Similarity 70.3%
Matches 173; Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  239 QGTKVEIKR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                         238 AGTKLELKR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-297-181-2
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                      Similarity
                                       174;
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  Query Match
Best Local
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                                       Matches
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Resistance
FILE REFRENCE: 0147-0189P
FILE REFRENCE: 0147-0189P
CURRENT APPLICATION NUMBER: US/09/419,788
CURRENT FILING DATE: 1999-10-18
EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER PILING DATE: 1998-10-16
EARLIER FILING DATE: 1998-10-16
SARLIER FILING DATE: 1998-10-16
SARLIER FILING DATE: 1998-10-16
SOFTWARE: PATENTION OF : 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Description of Artificial Sequence: synthetic, ; OTHER INFORMATION: natural origin US-09-419-788-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.7%; Score 905; DB 2; Length 267, 68.5%; Pred. No. 1e-66; Live 34; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09203958A
Patent No. 6682928
GENERAL INFORMATION
APPLICANT: GOLDSTEIN, Joel
APPLICANT: GOLDSTEIN, Joel
APPLICANT: GRAZIANO, Robert
APPLICANT: BED, Yashwant M.
TITLE OF INVENTION: BINDING COMPONENTS
FILE REPERENCE: MXI-0990CPA
CURRENT APPLICATION UNDER: US/09/203,958A
CURRENT FILING DATE: 1998-12-02
                       Sequence 30, Application US/09419788
Patent No. 6825325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTKVEIKRGLGGLVDYK 256
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240 GTKLELKRAVDAAAEQK 256
                                                                                     APPLICANT: FISCHER, Rainer
APPLICANT: SCHILLBERG, Stefan
APPLICANT: NAHRING, Jorg
APPLICANT: SACK, Markus
APPLICANT: MONECKE, Michael
APPLICANT: LIAO, Yu-Cai
APPLICANT: SIEGEL, Holger
APPLICANT: ZIMMERMAN, Sabine
APPLICANT: EMANS, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
US-09-419-788-30
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US-09-203-958A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 30
LENGTH: 267
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58 THYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----DPRGDDEPYWGQGT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHW 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 WLLQRPGQSPTRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 TSYNLKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCVRGVYYYGSSYEAFPYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 LVTVSAGGGGGGGGGGGGSDVVMTQTPLTLSITIGQPASISCKSSQSLLDSDGKTYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWINN----GN
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                                                                                                                                                                                                                                                                                                                             63.2%; Score 883; DB 2; Length 353;
66.1%; Pred. No. 8.9e-65;
tive 39; Mismatches 35; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Boque, Lluis
APPLICANT: Wichon, Dianne L.
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew 11.D.
ADDRESSEE: Townsend and Townsend and Crew 11.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
PRICE APPLICATION NUMBER: WO PCT/US97/02588
PRICE APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SUBBARION:
NAME: FAILS, SUBBARICH: 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
PRIOR APPLICATION NUMBER: 60/067232
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 353
                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic construct US-09-203-958A-4
                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 PPRTFGOGTKVEIK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:||| |||:|||
275 -PQTFGGGTKLEIK 287
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Matches 168; Conservative
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240 GTKVEIKR 247
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GTKLEIKR 245
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSPRILIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVBAEDIGVYYCMQGTHWPPRTFGQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 QSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYCAQNLE-IPRTFGG 354
                                                                                                                                                                                                                                                                                                                      3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                       AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDP-RGDDEPYWGQGTLVTVSSG
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                             DB 2; Length 365;
                                                                                                                                                                                                                                         Query Match 63.1%; Score 881.5; DB 2; Length Best Local Similarity 67.3%; Pred. No. 1.2e-64; Matches 167; Conservative 37; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTIONS: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
REFERENCE/DOCKET NUMBER: 015280-244100US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application US/08875811
Patent No. 6045793
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                                                   TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                       : 365 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 GTKVEIKR 247
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GTKLEIKR 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 GGGSCGGGGGSDIVLTQSPRSNPVTLGTSASISCRSTKSLLHSNGITYLYWYLQKPG 178
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APPLICANT: PISCHER, Rainer

APPLICANT: SCHILLBERG, Stefan

APPLICANT: SCHILLBERG, Stefan

APPLICANT: SCHILLBERG, Stefan

APPLICANT: SACK, Michael

APPLICANT: SACK, Michael

APPLICANT: SACK, Michael

APPLICANT: SIMMERMAN, Sabine

APPLICANT: EMANS, Neil

TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease

TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease

TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease

TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease

TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease

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TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.1%; Score 881.5; DB 2; Length 366; Best Local Similarity 67.3%; Pred. No. 1.2e-64; Matches 167; Conservative 37; Mismatches 37; Indels 7
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REFERENCE/DOCKET NUMBER: 015280-244100US
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                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-55
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61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDD----EPYWGQGTLVTV 116
                                                                                                                             86 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--WGGDGFYAMDYWGQGTLVTV 143
                                                                                                                                                                                              204 DWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQHYT 263
                                                                                                                                                                                                                                                                                           172 SWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTH 231
                         26 EVQLVESGGGIVQPGGSIRLSCAASGPTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 85
                                                                                                                                                                                                                        QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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Best Local Similarity 66.4%; Pred. No. 1.7e-63;
Matches 170; Conservative 36; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2020
TELEFRAK: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-09-490-070A-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 178, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Colin G. Sandercock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
                                                                                                                                                                                                                                                                                                                                                                                             232 WPPRTFGQGTKVBIKR 247
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
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                                                                                                                                            59 HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSS 118
                                                                                                                                                                        61 SYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAR-----PDVWGAGTLLLTVSA 114
                                                                                                                                                                                                                                              119 GGG---GSG----GGGSGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYL 171
                                                                                                                                                                                                                                                                       115 GAGPISGSGKPGPGEGSTKGAPDVLMTQAPL/ILSVTIGQPASISCKSSQSLLDGDGPGKTY1, 174
                                                                                                                                                                                                                                                                                                                                                                    172 SWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTH; 231
                                                                           1 MAEVQLQQSGAELVKPGASVKMSCKASGYTFTNYNMHWVKQTPGQGLEWIGAIYPRNGDT 60
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PAILLIN TO SOFTWARE: PAILLIN TO SOFTWARE: DAILLIN TO SOFTWARE: DAILLIN TO SOFTWARE: DAILLIN TO SOFTWARE: DAILLIN TO SOFTWARE: US/09/025,769B
FILLING DATE: 18-FEB-1998
PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 95 11 3021.0
APPLICATION NUMBER: EP 95 11 3021.0
ATTORNEY AGENT INFORMATION: NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: James F. Haley, Jr., Esq. c/o Fish & Neave
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
  33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 178, Application US/09025769B
Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 178:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 F-PHTFGGGTKLEIKR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                           232 WPPRTFGQGTKVEIKR 247
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amino acid
  171; Conservative
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Best Local Similarity 66.4
Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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  Matches
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Gaps

14;

Length 281; Indels

60

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144 SSAGGGGGGGGGGGGGGDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYL 203
                                                                                                                                   86 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--WGGDGFYAMDYWGQGTLVTV 143
                                                                                                                                                                                                                                                                                                        26 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                172 SWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTH
                                                                                                        61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDD-----EPYWGQGTLVTV
                      QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNTHY
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**TOPOLOGY: linear
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**MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-09-490-324-178
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NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 281 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                            264 TPP-TFGOGTKVEIKR 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.9%;
66.4%;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
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Best Local Similarity
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US-09-490-324-178
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                                                                                  AQKEQGRVIMITDISISIAYMELRSLRSDDIAVYYCARDPRGDD----EPYWGQGILVIV 116
                                                                                                           86 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--WGGDGFYAMDYWGQGTLVTV 143
                                                                                                                                                                                                                                                                                  204 DWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVBAEDVGVYYCQQHYT 263
                                                                                                                                                                         S----SGGGGGGGGGGGGGGGTVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYL 171
                                                                                                                                                                                                               144 SSAGGGGGGGGGGGGGGGGDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYL 203
                                                                                                                                                                                                                                                         SWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTH 231
  9
                        26 EVQLVESGGGLVQPGGSLRLSCAASGPTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 85
QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plucckhun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.9%; Score 866; DB 2;
66.4%; Pred. No. 1.7e-63;
iive 36; Mismatches 36
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FILING DATE: 18-FEB-1998
APPLICATION WUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-09-490-153-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 178, Application US/09490153 Patent No. 6706484 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: (212)596-9090
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LENGTH: 281 amino acids
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                                                                                                                                                                                                                                                                                                                                              232 WPPRIFGQGTKVEIKR 247
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Best Local Similarity 66.4%
Matches 170; Conservative
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STATE: New York
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
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COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
Sequence 178, Application US/09490324
; Sequence 1682422
; GENERAL INFORMATION:
    APPLICANT: Knapplk, Achim
    APPLICANT: Knapplk, Achim
    Ilag, Vic
    Ge, Liming
    Moroney, Simon
    TITLE OF INVENTION: Protein/(Poly)peptide libraries
    NUMBER OF SEQUENCES: 373
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Pred. No. 1.7e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION:
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APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Winter, Gregory
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICANTON NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDE----PYWGQGTLV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 TVSSGGGGGGGGGGGGGGSDIELTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 QQRPQQSPRRLIXKVSNRDSGVPDRFSGSGSGTDFTLKISRVBAEDIGVYYCMQGTHWPP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 TVSSGGGGGGGGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWINNG----NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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60.8%; Score 850; DB 2; Length 249;
Best Local Similarity 64.8%; Pred. No. 3.1e-62;
Matches 164; Conservative. 35; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: scFv form of the anti-oxazalone antibody US-09-726-219A-190
                                                                                                                                                                                          APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PLING DATE: 2007-10
PRIOR PLING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR PLING DATE: 1990-10-19
PRIOR PLING DATE: 1990-10-19
PRIOR PLING DATE: 1990-10-19
PRIOR PLING DATE: 1990-11-12
PRIOR PLING DATE: 1990-11-12
PRIOR PLING DATE: 1990-11-12
PRIOR PLING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR PLING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR PLING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR PLING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR PLING DATE: 1993-01-08
PRIOR PLING DATE: 1993-01-08
PRIOR PLING DATE: 1993-01-08
PRIOR PLING DATE: 1993-01-08
                                                                                                                  Sequence 190, Application US/09726219A
Patent No. 6806079
                                                                                                                                                                                                                                                                                                                 Johnson, Kevin
Hoogenboom, Hendricus
Griffiths, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Jackson, Ronald
Holliger, Kasper
Marks, James
240 GGGTKLEIKR 249
                                                                                                                                                                                                                                                                                          Pope, Anthony
                                                                                           US-09-726-219A-190
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APPLICANT:
APPLICANT:
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APPLICANT: Scheiflinger, Friedrich
APPLICANT: Kerschbaumer, Randolf
APPLICANT: Feakcher, Falko-Guenter
APPLICANT: Former, Friedrich
APPLICANT: Baxter Aktiengesellschaft
ITILE OF INVENTION: Pactor IX/Factor IXa Activating Antibodies and Antibody
ITILE OF INVENTION: Derivatives
FILE REPERENCE: 20695C-005900US
CURRENT APPLICATION NUMBER: US/09/661,992B
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: AT A157600
PRIOR FILING DATE: 1999-09-14
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                                                                                                                                                                        86 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--WGGDGFYAMDYWCQGTLVTV 143
                                                                                                                                                                                                                                                                    61 PDSVRGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SGGGSGGRASGGGGSQIVLTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AQKPQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARD---PRGDDEPYWGQGTLVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGGGGSGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTF 237
                                                                                           85
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                                                                       26 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                             61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDD----EPYWGQGTLVTV
                                               3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWINNGN--THY
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
FOTHER INFORMATION: Description of Artificial Sequence:scFv from US-09-661-992B-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.2%; Score 856; DB 3; Length 249; Best Local Similarity 65.2%; Pred. No. 9.9e-63; Matches 163; Conservative 38; Mismatches 43; Indels
Indels
  36;
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 84, Application US/09661992B
Patent No. 7033590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 TPP-TFGQGTKVEIKR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPPRIFGQGTKVEIKR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 84
LENGTH: 249
TYPE: PRT
ORGANISM: Artificial Sequence
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-661-992B-84
170;
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Matches
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APPLICANT: Winter, Gregory
APPLICANT: Winter, Timothy
APPLICANT: Winter, Timothy
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00004
CURRENT APPLICATION NUMBER: US/09/196,522
CURRENT APPLICATION NUMBER: US 9015198.6
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR PILING DATE: 1990-10-19
PRIOR PILING DATE: 1990-10-19
PRIOR PELING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 902450.3
PRIOR APPLICATION NUMBER: GB 9110474.9
PRIOR APPLICATION NUMBER: GB 911044.9
PRIOR PELING DATE: 1991-05-06
PRIOR FILING DATE: 1991-07-10
PRIOR PELING DATE: 1991-07-10
PRIOR PELING DATE: 1993-05-15
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1993-07-10
PRIOR FILING DATE: 1993-07-08
PRIOR PELING DATE: 1993-07-08
PRIOR PELING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PARENTIN VARIET: US 08/484,893
PRIOR PLING DATE: 1993-01-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 TVSSGGGGGGGGGGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWF 174
178 LQKPGQSPKLLIYKVSNRFSGVPDRFSGSGGGTDFTLKISRVEAEDLGVYYCFQGSH-VP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGGGLVQPGGSLRLSCATSGFTFSNYYMGWVRQPPGKALEWLGSVRNKVNGYTT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Gaps
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; OTHER INFORMATION: scFv form of the anti-oxazalone antibody NQ11
US-09-196-522-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
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60.8%; Score 850; DB 2;
Best Local Similarity 64.8%; Pred. No. 3.1e-62;
Matches 164; Conservative 35; Mismatches 42.
                                                                                                                                                                                                                                                                                                                            Sequence 190, Application US/09196522
Patent No. 6916605
GENERAL INFORMATION:
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Griffiths, Andrew
Jackson, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holliger, Kasper
Marks, James
Clackson, Timothy
Chiswell, David
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ORGANISM: Artificial Sequence
                                                                                                                   237 YTFGGGTKLEIKR 249
                                                                         235 RTFGOGTKVEIKR 247
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US-11-056-825-2
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration
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US-11-056-825-8
US-11-056-825-8
US-10-257-864A-92
US-10-138-505-26
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US-10-645-085A-90
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US-10-645-085A-90
US-10-138-505-30
US-10-23-418-1991
US-10-293-418-1991
US-11-056-444-1991
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US-11-138-505-30
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Maximum Match 100%
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APPLICANT: Felding-Habermann, Brunhilde
APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Janda, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-042
CURRENT APPLICATION NUMBER: US/11/056,825
CURRENT PILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/544,807
PRIOR APPLICATION NUMBER: US 60/544,807
RICH APPLICATION NUMBER: US 60/544,807
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US-10-399-585-119

US-10-645-085A-91

US-10-138-505-34

US-10-257-864A-93

US-10-399-518-122

US-10-399-585-121

US-10-399-585-121

US-10-399-585-124

US-10-399-588-124

US-10-399-588-124

US-10-399-588-124

US-10-399-588-124

US-10-399-588-124

US-10-399-588-124

US-10-399-588-124

US-10-399-656-47

US-10-239-656-49

US-10-239-656-49

US-10-339-656-49

US-10-339-656-49

US-10-339-656-49

US-10-339-656-49
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Best Local Similarity 100.
Matches 261; Conservative
  ORGANISM: Artificial
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Sequence 7, Application US/11056825;
Bublication No. US20050255109A1
GENERAL INFORMATION:
APPLICANT: Felding-Habermann, Brunhilde
APPLICANT: Saven, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-0042
CURRENT APPLICATION NUMBER: US/11/056,825
CURRENT APPLICATION NUMBER: US/0626,726
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR APPLICATION NUMBER: US 60/544,807
PRIOR PALING DATE: 2004-01.13
PRIOR PALING DATE: 2004-01.3
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
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; Beduence 1964, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
    APPLICANT: Ruben et al.
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
    TIER EMPERENCE: PF523
    CURRENT APPLICATION NUMBER: US/09/880,748
    CURRENT FILING DATE: 2001-06-15
    PRIOR APPLICATION NUMBER: 60/212,210
    PRIOR APPLICATION NUMBER: 60/212,210
    PRIOR APPLICATION NUMBER: 60/210,816
    PRIOR PILING DATE: 2000-10-17
    PRIOR FILING DATE: 2001-03-16
    PRIOR FILING DATE: 2001-03-21
    PRIOR APPLICATION NUMBER: 60/277,379
    PRIOR APPLICATION NUMBER: 60/277,379
    PRIOR APPLICATION NUMBER: 60/277,379
    PRIOR FILING DATE: 2001-03-21
    PRIOR FILING DATE: 2001-03-21
    PRIOR FILING DATE: 2001-03-21
    PRIOR FILING DATE: 2001-03-25
    NUMBER OF SEQ ID NOS: 3239
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ORGANISM: Artificial
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61 AQKFQGRVTMTTDTSTSTAYMBLRSLRSDDTAVYYCARDPRGDDE-----PYWGQGTLVT.115
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PP523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-010-17
PRIOR PILING DATE: 2000-010-17
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PRIOR PILING DATE: 2000-010-17
PRIOR PILING DATE: 2000-06-16
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; Pred. No. 2.8e-74;
15; Mismatches 10;
                                                                                                                                                                                            81.2%; Score 1135; DB 3;
86.2%; Pred. No. 2.8e-74;
tive 15; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1964, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
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86.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 PFTFGQGTKMEIKR 253
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1964
LENGTH: 253
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Best Local Similarity 86.2
Matches 219; Conservative
                                                                                                                                                                                                                                                      Conservative
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SEQ ID NO 1964
                                                                                                                    sapiens
                                                                                                                                                                                                                         Similarity
                                                                                                           ; ORGANISM: Homo
US-09-880-748-1964
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                                                                                                                                                                                         Query Match
Best Local Simi:
Matches 219;
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us-11-056-825-2.rapbm

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181 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQATRW- 239
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81.2%; Score 1135; DB 6;
Best Local Similarity 86.2%; Pred. No. 2.8e-74;
Matches 219; Conservative 15; Mismatches 10;
                                                                                                                              Sequence 1964, Application US/11266444 Publication No. US20060062789A1 GENERAL INFORMATION:
                             234 PRIFGQGTKVEIKR 247
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                                               ORGANISM: Homo sapiens
                                                                                                               US-11-266-444-1964
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                61 AQKLQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCARNPYYYDSSEGFFDYWGQGTWVT 120
                                                                       61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDE-----PYWGQGTLVT 115
                                                                                                               FOORPGOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWP 233
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                                                        VSSGGGGGGGGGGGGG--EIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSW
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Best Local Similarity 86.2%; Pred. No. 2.8e-74;
Matches 219; Conservative 15; Mismatches 10; Indels 10; Gaps
                                                                                                                                                                        234 PRTFGQGTKVEIKR 247
                                                                                                                                                                                         240 PFTFGQGTKMEIKR 253
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ORGANISM: Homo sapiens
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US-11-054-515-1964
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PAPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator)
FILE REPREBRÜGE: PES23PIDI
CURRENT APPLICATION NUMBER: US/11/266,444

CURRENT FILING DATE: 2005-11-04

PRIOR PILING DATE: 2001-06-16

PRIOR PILING DATE: 2000-06-16

PRIOR PILING DATE: 2000-06-16

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-3-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

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Sequence 4, Application US/11056825

Sequence 4, Application No. US20050255109A1

Sequence 4, Application No. US20050255109A1

SERNEAL INFORMATION:

APPLICANT: Felding-Habermann, Brunhilde

APPLICANT: Saven, Alan

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS

FILE REFERENCE: SCRP-0042

CURRENT APPLICATION NUMBER: US/11/056,825
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGSGGGGSGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |------GGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSV----SSSYLAWYQQKP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQ-GTHWPPRTF 237
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APPLICANT: Felding-Habermann, Brunhilde
APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Janda, Mim D.
APPLICANTON: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-0042
CURRENT APPLICATION NUMBER: US/11/056,825
CURRENT FILING DATE: 2005-02-11
PRIOR FILING DATE: 2004-11-10
RICA APPLICATION NUMBER: US 60/544,807
RICA RAPLICATION NUMBER: US 60/544,807
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                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                         Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                   27; Indels
                                                                                                                                                                                                                                                                                                                                  68.9%; Score 963; DB 6;
72.0%; Pred. No. 7.7e-62;
tive 29; Mismatches 27
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/544,807
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.3
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OTHER INFORMATION: Synthetic Construct
US-11-056-825-4
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US-11-056-825-8
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Publication No. US20050255109A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Query Match 68.9
Best Local Similarity 72.0
Matches 190; Conservative
                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial
                                                                                                                                              SEQ ID NO 4
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Best Local 8
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Matches
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                                                       61 NSAQOFQGRVTWTRDTSISTAYMELSRLRSDDTAMYYCARPPRGDGPDYWGQGTLVTVSS 120
                                                                                                                                                        G------GGGGSEIVLIQSPGTLSLSPGERATLSCRASQSV---SSSYLAWYQQXP 167
                                                                                                                                                                                                                                                                                 59 HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPY--WGQGTLVTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 SSGGGGGGGGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSGGGGGGGGGGGBDVVMTQSPLSLPVSLGDQASISCRSSQSLVHSNGKTYLHWYLQ
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HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSS
                                                                                                                     GGGGGGGGGGGGGTVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRP
                                                                                                                                                                                                                                          179 GQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQ-GTHWPPRTF
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US-10-257-864A-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/JP01/03288
PRIOR PELING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: PCT/JP01/01912
PRIOR APPLICATION NUMBER: PCT/JP01/01912
PRIOR APPLICATION NUMBER: JP2000-115246
PRIOR APPLICATION NUMBER: JP2000-115246
PRIOR PELING DATE: 2000-04-17
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: JP2000-321822
PRIOR PILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/257,864A CURRENT FILING DATE: 2003-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OH-EDA, MAGAYOSHI
APPLICANT: UNO, SHINSUKE
APPLICANT: KIUCHI, YASUFUNI
APPLICANT: GOTEMBA-SHI, OHTOMO
TITLE OF INVENTION: AGONIST ANTIBODIES
FILE REFERENCE: 065678-0107
                                                                                                                                                                                                                                                                                                                                                                                                         226 GQGTKVDIKRGLGGLVDYKDDD 247
                                                                                                                                                                                                                                                                                                                                                                        GQGTKVEIKRGLGGLVDYKDDD 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASAYUKI
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SSGGGGGGGGGGGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQ 176
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## APPLICANT: KIKUCHI, Yasufumi
## TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV
## FILE REPERENCE: 06578/0102
## CURRENT APPLICATION NUMBER: US/10/138,505
## CURRENT FILING DATE: 2002-05-06
## PRIOR PLILATION NUMBER: US/09/523,095
## PRIOR PLILATION NUMBER: JP 11-6357
## PRIOR PLILATION NUMBER: JP 11-6357
## PRIOR PLILATION NUMBER: JP 11-6357
## PRIOR PLILATION NUMBER: JP 11-6357
## PRIOR PLILATION NUMBER: JP 11-6357
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APPLICANT: TSUCHIYA, MASAYUKI
APPLICANT: TSUCHIYA, MASAYUKI
APPLICANT: UNO, SHINSUKE
APPLICANT: WINO, SHINSUKE
APPLICANT: GYTENGHE, YASUFUMI
APPLICANT: GYTENGHE, TSUCHIYOMO
TITLE REFERENCE: 055678-0107
CURRENT APPLICATION NUMBER: US/10/257,864A
CURRENT FILING DATE: 2003-07-24
FRIOR APPLICATION NUMBER: PCT/JPO1/03288
FRIOR APPLICATION NUMBER: PCT/JPO1/03288
FRIOR PILING DATE: 2001-04-17
FRIOR FILING DATE: 2000-04-17
FRIOR FILING DATE: 2000-04-17
FRIOR FILING DATE: 2000-04-17
FRIOR APPLICATION NUMBER: JP2000-115246
FRIOR APPLICATION NUMBER: JP2000-115246
FRIOR APPLICATION NUMBER: JP2000-321821
FRIOR APPLICATION NUMBER: JP2000-321821
FRIOR APPLICATION NUMBER: JP2000-321821
FRIOR APPLICATION NUMBER: JP2000-321822
FRIOR APPLICATION NUMBER: JP2000-321822
FRIOR APPLICATION NUMBER: JP2000-321822
FRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PATENTIN VET: 2.1
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LENGTH: 274
TYPE: PRT
ORGANISM: Mus musculus
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US-10-138-505-26
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Best Local Similarity 69.8%; Pred. No. 1.2e-59;
Matches 185; Conservative 31; Mismatches 34; Indels 15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FUNCHINA, NACSHI
APPLICANT: TSUCHIYA, MASAYUKI
APPLICANT: TSUCHIYA, MASAYUKI
APPLICANT: UNC. SHINSUKE
APPLICANT: UNC. SHINSUKE
APPLICANT: UNC. SHINSUKE
APPLICANT: OTHOMO, SHINSUKE
APPLICANT: KIKUCHI, YASUFUMI
APPLICANT: OTHOMO, SHINSUKE
TITLE OF INVENTION: AGONIST ANTIBODIES
FILE REFERENCE: 065678-0108
CURRENT APPLICATION NUMBER: US/10/645,085A
CURRENT APPLICATION NUMBER: PCT/JPO1/03288
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: JP 2000-321821
PRIOR APPLICATION NUMBER: JP 2000-321821
PRIOR APPLICATION NUMBER: JP 2000-321821
PRIOR APPLICATION NUMBER: JP 2000-321821
PRIOR APPLICATION NUMBER: JP 2000-321822
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: JP 2000-321822
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PRIOR APPLICANTON NUMBER: JP 2000-321822
                                                                                        257 FGGGTKLEIK-----DYKDDDDK 274
                 237 FGGGTKVEIKRGLGGLVDYKDDDDK 261
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                                                                                                                                                                                                                                                                                                   ; Sequence 92, Application US/10645085A; Publication No. US20040258684A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/10138505
Publication No. US20030108546A1
GENERAL INFORMATION:
APPLICANT: FUKUSHIMA, Naoshi
APPLICANT: UNO, Shinsuke
APPLICANT: OH-EDA, Masayoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                    US-10-645-085A-92
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LENGTH: 274
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177 RPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRT 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.5%; Score 929.5; DB 5 69.1%; Pred. No. 2.2e-59;
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FUGUSHIMA, MAGSHI
APPLICANT: FUGUSHIMA, MASAYUKI
APPLICANT: UNO, SHINSTER
APPLICANT: UNO, SHINSTER
APPLICANT: OHTOWO, TOSHIHIKO
APPLICANT: OHTOWO, TOSHIHIKO
APPLICANT: TSUNODA, HIROYUKI
ITILE OF INVENTION: DEGRADED AGONIST ANTIBODY
FILE REFERENCE: 065678/0112
CURRENT APPLICATION NUMBER: US/10/399,585
CURRENT APPLICATION NUMBER: PCT/JP01/09260
PRIOR FILING DATE: 2001-022
PRIOR PELING DATE: 2001-022
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
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US-10-645-085A-90
'S Sequence 90, Application US/10645085A
'Publication No. US20040258684A1
                                                                                                                                                                                                                                                                                          Sequence 118, Application US/10399585
Publication No. US20040242847A1
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US-10-399-585-118
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                                                                                                                                                              Gaps
                                                                                                        tch 66.5%; Score 929.5; DB 4; Length 274; al Similarity 69.1%; Pred. No. 2.2e-59; 183; Conservative 32; Mismatches 35; Indels 15;
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                              SEQ ID NO:
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Publication No. US20040091475A1
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, MASAVUKI
APPLICANT: TSUCHIYA, MASAVUKI
APPLICANT: TSUCHIYA, MASAVUKI
APPLICANT: TSUCHOA, HROUND
APPLICANT: TSUCHOA, HROUND
APPLICANT: TSUCHOA, HIROVUKI
APPLICANT: TSUCHOA, HIROVUKI
APPLICANT: ORITA, TETSURO
TITLE OF INVENTION: DESCRADED TPO AGONIST ANTIBODY
FILE REFERENCE: 065678/0111
CURRENT FILING DATE: 2003-09-25
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: UP 2001-277314
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
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PRIOR FILING DATE: 2001-09-13
; FEATURE:
; OTHER INFORMATION: amino acid sequence encoded by
US-10-257-864A-90
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US-10-399-518-119
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Query Match 66.5%; Score 929.5; DB 5; Length 274; Best Local Similarity 69.1%; Pred. No. 2.2e-59; Matches 183; Conservative 32; Mismatches 35; Indels 15; Gaps
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APPLICANT: TSUCHINA, NAOSHI
APPLICANT: TSUCHINA, MAGAYUKI
APPLICANT: OH-BDA, MAGAYOKHI
APPLICANT: OH-BDA, MAGAYOKHI
APPLICANT: OHO-BDA, MAGAYOKHI
APPLICANT: OHO-BDA, MAGAYOKHI
APPLICANT: OHTOWO, TOSHIHIKO
TITLE OF INVENTION: AGONIST ANTIBODIES
FILE REFERENCE: 065678-0108
CURRENT APPLICATION NUMBER: US/10/645,085A
CURRENT APPLICATION NUMBER: PCT/JPO1/01288
PRIOR PILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2000-03-12
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2000-04-17
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PRIOR PILING DATE: 2000-04-17
PRIOR PILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: JP 2000-321821
PRIOR PILING DATE: 2000-0-20
PRIOR APPLICATION NUMBER: JP 2000-321822
PRIOR APPLICATION NUMBER: JP 2000-321822
PRIOR PILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PALENTIN VOY: 13.2
LENGTH 274
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ORGANISM: Mus musculus
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59 HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPY--WGQGTLVTV 116 1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNT 58 δ ò ò

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177 RPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRT 236

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Search completed: August 9, 2006, 13:30:14 Job time : 180 secs

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Similarity
US-11-337-300-278
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US-11-337-300-278
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214, App
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 GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-155-444-2
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Maximum Match 100%
Listing first 45 summaries
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        US-11-337-300-272
        Sequence 272, Appl 28

        27
        764.5
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        US-11-183-325-20
        Sequence 20, Appl 29

        28
        764.5
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        US-11-337-300-252
        Sequence 25.3
        Appl 20

        30
        763.5
        54.6
        279
        6
        US-10-968-757-2
        Sequence 25.4
        Appl 30

        31
        761
        54.6
        252
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        US-11-337-300-26
        Sequence 26.4
        Appl 30

        32
        761
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        US-11-337-300-26
        Sequence 26.4
        Appl 30

        34
        761
        54.4
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        US-11-337-300-26
        Sequence 28.6
        Appl 30

        35
        759.5
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        248
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        US-11-337-300-28
        Sequence 27.6
        Appl 30

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        US-11-337-300-226
        Sequence 27.6
        Appl 30

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        US-11-337-300-226
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ALIGNMENTS

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Sequence 278, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: ter Meulen, Jan H.
APPLICANT: De Kruif, Cornelis A.
APPLICANT: van den Brink, Edward N.
APPLICANT: WINGERICH GOND
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REPERENCE: 0091 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/337,300
CURRENT FILING DAFFE: 2006-01-20
NUMBER OF SED ID NOS: 478
SOFTWARE: PatentIn version 3:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 SWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTH 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDP-----RGDDEPYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 LVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGTVLGQPASISCRSSQNLVYSDGNTYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.5%; Score 943; DB 7; Length 256; 74.2%; Pred. No. 2.1e-62; ive 19; Mismatches 35; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: SC03-053
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240 -TPLTFGQGTRLEIKR
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Matches 190; Conservative
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SEQ ID NO 2
LENGTH: 697
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                                                              ; OTHER INFORM US-11-155-444-2
                                                                                                                  Query Match
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                                                Publication No. US20060121580A1
GENERAL INFORMATION:
APPLICANT: Crucall Holland B.V.
APPLICANT: Treal Holland B.V.
APPLICANT: The Kruif, Cornelis A.
APPLICANT: Van den Brink, Edward N.
APPLICANT: Goudsmit, Jany
TITLE OF INVENTYON: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: Patentin Version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TSYAQKFQGRVTLTRDTSTSTVYMELSSLRSEDTAVYYCARFPGGTRSRGYMDVMGKGTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GARBER, ELLEN
APPLICANT: GARBER, ELLEN
APPLICANT: BAILLY, VERONIQUE
APPLICANT: BAILLY, VERONIQUE
APPLICANT: BRILLY, VERONIQUE
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
FILE REFERENCE: BGNA168CN
CURRENT APPLICATION NUMBER: US/11/155,444
CURRENT APPLICATION NUMBER: DCT/USO3/041393
PRIOR PILING DATE: 2005-06-17
PRIOR PELLING DATE: 2005-12-22
PRIOR PELLING DATE: 2002-12-20
PRIOR PELLING DATE: 2002-12-20
PRIOR PELLING DATE: 2002-12-20
PRIOR PELLING DATE: 2002-12-20
PRIOR PELLING DATE: 2002-12-20
PRIOR PELLING DATE: 3002-12-20
SPRIOR PILING DATE: 3002-12-30
SOFTWARE: PAECHIN VEY: 3.3
SOFTWARE: PAECHIN VEY: 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.7%; Score 863; DB 7; Length 252; Best Local Similarity 68.6%; Pred. No. 1.6e-56; Matches 175; Conservative 26; Mismatches 40; Indels
                                      ; Sequence 290, Application US/11337300
; Publication No. US20060121580A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/11155444 Publication No. US20060104971A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 PP-AFGGGTKVEIKR 250
                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SC03-059
US-11-337-300-290
RESULT 2
US-11-337-300-290
                                                                                                                                                                                                                                                                                                           SEQ ID NO 290
LENGTH: 252
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APPLICANT: LEPAGE, DOREEN
APPLICANT: GILL, ALAN
AITHE OF INVENTION: LYMPHOTOXIN BETA RECEPTOR AGENTS IN COMBINATION WITH
TITLE OF INVENTION: CHEMOTHERAPEUTIC AGENTS
FILE REPERENCE: BGNA171CN
CURRENT APPLICATION NUMBER: US/11/156,109
CURRENT APPLICATION NUMBER: 005-06-17
PRIOR PILLING DATE: 2003-12-22
PRIOR PILLING DATE: 2003-12-22
PRIOR FILLING DATE: 2002-12-20
PRIOR PILLING DATE: 2002-12-20
PRIOR FILLING DATE: 2002-12-20
PRIOR FILLING DATE: 2002-12-20
PRIOR FILLING DATE: 2002-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                           180 OSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQ
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                                                                             OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of OTHER INFORMATION: huCBE11/huBHA10 bispecific-1 antibody construct
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                    60.5%; Score 846; DB 7; Length 697; 67.2%; Pred. No. 7.7e-55; Live 28; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.5%; Score 846; DB 7; Length 697; Best Local Similarity 67.2%; Pred. No. 7.7e-55; Matches 166; Conservative 28; Mismatches 43; Indels
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; Sequence 2, Application US/11156109
; Publication No. US20060134102Al·
; GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                    Best Local Similarity 67.29
Matches 166; Conservative
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SOFTWARE: PatentIn Ver. 3.3
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                                                                                                                  GGGSGGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPG 179
                         60 YAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDBPYWGQGTLVTVSSG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GARGER, GLIEN
APPLICANT: BAILLY, VERONIQUE
APPLICANT: BAILLY, VERONIQUE
APPLICANT: BROWNING, JEFFREY L.
TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
FILE REFERENCE: BGNA166CN
CURRENT PELICATION NUMBER: US/11/155,444
CURRENT FILING DATE: 2005-06-17
PRIOR FILING DATE: 2003-12-22
PRIOR FILING DATE: 2003-12-22
PRIOR FILING DATE: 2003-12-20
PRIOR PILING DATE: 2003-12-20
PRIOR PILING DATE: 2003-12-20
PRIOR PILING DATE: 2003-12-20
PRIOR PILING DATE: 2003-12-20
PRIOR PILING DATE: 2002-12-20
PRIOR PILING DATE: 2003-12-20
PRIOR PILING DATE: 2002-12-20
PRIOR PILING DATE: 2002-12-20
                                                                                        180 QSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVBAEDIGVYYCMQGTHWPPRTFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: huCBE11/huBHA10; OTHER INFORMATION: bispecific-2 antibody construct
US-11-155-444-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWINNGNTH--
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                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/11155444
Publication No. US20060104971A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GARBER, ELLEN
                                                                                                                                                                                                         240 GTKVEIK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTKVEIK 246
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LENGTH: 731
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-11-155-444-6
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Sequence 6, Application US/11156109 Publication No. US20060134102A1 GENERAL INFORMATION:

US-11-156-109-6

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APPLICANT: GILL, ALAN
TITLE OF INVENTION: LYMPHOTOXIN BETA RECEPTOR AGENTS IN COMBINATION WITH
TITLE OF INVENTION: LYMPHOTOXIN BETA RECEPTOR AGENTS
TITLE OF INVENTION: CHEMOTHERAPEUTIC AGENTS
FILE REPERBACE: BGNA17LM
CURRENT APPLICATION NUMBER: US/11/156,109
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: PCT/US03/041243
PRIOR APPLICATION NUMBER: 60/435,185
PRIOR PILING DATE: 2002-12-20
PRIOR PILING DATE: 2002-12-20
PRIOR PILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 14
SOFTWARR: PATENTIN OFE: 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493 SQVQLVQSGAEVKKPGSSVKVSCKASGYTFTTYYLHWVRQAPGQGLEWMGWIYPGNVHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GGGSGGGGGGGBIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 YAQKEQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSSG
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APPLICANT: RING, D.
APPLICANT: RING, D.
APPLICANT: OPPERMENT, H.
TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING FILE REFERENCE: CIBT-P01-130
CURRENT PAPLICATION NUMBER: US/10/684,237
CURRENT PILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US/09/558,741
PRIOR APPLICATION NUMBER: 07/831,967
PRIOR FILING DATE: 1992-02-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: hCBE11/hBHA10 OTHER INFORMATION: bispecific-1 antibody construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.5%; Score 846; DB 7; Length 731; Best Local Similarity 67.2%; Pred. No. 8.1e-55; Matches 166; Conservative 28; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
APPLICANT: LEPAGE, DOREEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 731
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LENGTH: 252
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Matches 154; Conservative
232 VVFGGGTKLTV 242
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232 GGTKLEIKR 241
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: human
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US-11-337-300-216
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US-10-539-402-32
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LENGTH: 254
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                                                                                                                                                                                                                                                                                                                                                                                  GGGSGGGGSGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPG 179
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                                                                                             Query Match 58.2%; Score 813; DB 6; Length 252; Best Local Similarity 63.5%; Pred. No. 7.5e-53; Matches 160; Conservative 40; Mismatches 46; Indels
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66.5%; Pred. No. 1.2e-52;
tive 20; Mismatches 48
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; OTHER INFORMATION: 26-10 sFv'
US-10-684-237-4
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US-11-337-300-65
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GTKLEIKRSGGG 250
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Best Local Similarity 66.5
Matches 167; Conservative
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Sequence 216, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: ter Meulen, Jan H.
APPLICANT: van den Brink, Edward N.
APPLICANT: van den Brink, Edward N.
APPLICANT: Van den Brink, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 MITDISISIAYMELRSLRSDDTAVYYCARD-----PRGDDEPYWGQGTLVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 SGGGGGGGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVBAEDIGVYYCMQGTHWPPRTF 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 EVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNTHYAQKFQGRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.2%; Score 799.5; DB 6; 61.6%; Pred. No. 7.2e-52;
Sequence 32, Application US/10539402
Publication No. US2006011547741
GENERAL INFORMATION:
APPLICANT: Tufts University
TITLE OF INVENTION: Houropilin-1 Inhibitor
FILE REFERENCE: XE12EPC
CURRENT APPLICATION NUMBER: US/10/539,402
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 60/435,893
PRIOR APPLICATION NUMBER: US 60/435,893
PRIOR APPLICATION NUMBER: EP 03000615
PRIOR APPLICATION NUMBER: EP 03000615
PRIOR APPLICATION NUMBER: 2003-01-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE PRICED DATE: 2003-01-15
NUMBER PRICED DATE: 2003-01-15
NUMBER PRICED DATE: 2003-01-15
NUMBER PRICED DATE: 2003-01-15
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us-11-056-825-2.rapbn

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34; Mismatches
                                                                                                                Sequence 242, Application US/11337300
Publication No. US20060121580Al
GENERAL INFORMATION:
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                                                                                                                                                                               APPLICANT: Crucell Holland B.V.
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LEWOTH: 254
TYPE: PRT
ORGANISM: Artificial sequence
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; OTHER INFORMATION: SC03-035
US-11-337-300-242
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Best Local Similarity 62.73
Matches 158; Conservative
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APPLICANT: ter Meulen, Jan H.
APPLICANT: ter Meulen, Jan H.
APPLICANT: van den Brink, Edward N.
APPLICANT: Goudsmit, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT PAPLICANT: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                    HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEP--YWGQGTLVTV 116
                                                                                                                                                                                                                                                                                                    SSGGGGGGGGGGGGGS-EIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGN-TYLSWF 174
                                                                                                                                                                                                                                                                                                                                                                                                      181 QQXPGQPPKLLIYWASTRQSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPP 240
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                                                                                                                                        1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWINNGN--T
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                                                         Query Match 56.6%; Score 791; DB 7; Length 254; Best Local Similarity 63.2%; Pred. No. 3.1e-51; Matches 160; Conservative 33; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 254;
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Pred. No. 7.3e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 284, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
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Best Local Similarity 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 RTFGQGTKVEIKR 247
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US-11-337-300-284
  ; OTHER INFORMATION: SC03-021
US-11-337-300-216
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APPLICANT: ter Meulen, Jan H.
APPLICANT: ter Meulen, Jan H.
APPLICANT: be Kruif, Cornelis A.
APPLICANT: van den Brink, Edward N.
APPLICANT: dand den Brink, Edward N.
APPLICANT: Goudsmit, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
FURRENT APPLICATION NUMBER: US/11/337,300
CURRENT APPLICANTION NUMBER: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Crucell Holland B.V.
APPLICANT: Crucell Holland B.V.
APPLICANT: ter Meulen, Jan H.
APPLICANT: van den Brink, Edward N.
APPLICANT: van den Brink, Edward N.
APPLICANT: Goudemit, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT PILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: PATENTIN version 3.1
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TYPE: PRT
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                                                                                                                                               2 MAQMQLVQSGTEVKKPGESLKISCKGSGYGFITYWIGWVRQMPGKGLEWMGIIYPGDSET 61
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$; Pred. No. 1.2e-50;

33; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 276, Application US/11337300 Publication No. US20060121580A1 GENERAL INFORMATION: APPLICANT: Crucell Holland B.V.
                                                            56.0%;
63.2%;
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; FEATURE:
; OTHER INFORMATION: SC03-022
US-11-337-300-218
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US-11-337-300-276
                                                        Query Match
Best Local Similarity 63.2<sup>3</sup>
Matches 160; Conservative
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Matches 159; Conservative
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US-11-337-300-276
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APPLICANT: ter Meulen, Jan H.
APPLICANT: ter Meulen, Jan H.
APPLICANT: be Kruif, Cornelis A.
APPLICANT: van den Brink, Edward N.
APPLICANT: van den Brink, Edward N.
APPLICANT: Goudsmit, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REPREBENCE: 0091 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/337,300
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: Patentin version 3.1
SEQ ID NO 274
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                                                                                                                                                                                    Sequence 274, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          APPLICANT: Crucell Holland B.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
235 RIFGQGTKVEIKR 247
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US-11-337-300-274
                                                   240 YTFGQGTKVEIKR
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Job time : 33 secs
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RESULT 1
PCT-USOS-04612-2
PCT-USOS-02, Application PC/TUSOS04612
; GENERAL INFORMATION:
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                                                                                                                                                                                        9, 2006, 13:15:37 ; Search time 603 Seconds (without alignments) 660.921 Million cell updates/sec
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1: / EMC_Celerra_SIDS3/ptodata/2/paa/PGG6_COMB.pep:*

2: / EMC_Celerra_SIDS3/ptodata/2/paa/USG16_COMB.pep:*

3: / EMC_Celerra_SIDS3/ptodata/2/paa/USG73_COMB.pep:*

4: / EMC_Celerra_SIDS3/ptodata/2/paa/USG73_COMB.pep:*

5: / EMC_Celerra_SIDS3/ptodata/2/paa/USG76_COMB.pep:*

7: / EMC_Celerra_SIDS3/ptodata/2/paa/USG76_COMB.pep:*

8: / EMC_Celerra_SIDS3/ptodata/2/paa/USG76_COMB.pep:*

9: / EMC_Celerra_SIDS3/ptodata/2/paa/USG76_COMB.pep:*

10: / EMC_Celerra_SIDS3/ptodata/2/paa/USG76_COMB.pep:*

11: / EMC_Celerra_SIDS3/ptodata/2/paa/USG86_COMB.pep:*

13: / EMC_Celerra_SIDS3/ptodata/2/paa/USG86_COMB.pep:*

14: / EMC_Celerra_SIDS3/ptodata/2/paa/USG86_COMB.pep:*

15: / EMC_Celerra_SIDS3/ptodata/2/paa/USG86_COMB.pep:*

16: / EMC_Celerra_SIDS3/ptodata/2/paa/USG86_COMB.pep:*

17: / EMC_Celerra_SIDS3/ptodata/2/paa/USG86_COMB.pep:*

18: / EMC_Celerra_SIDS3/ptodata/2/paa/USG86_COMB.pep:*

18: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

19: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

10: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

10: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

11: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

12: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

13: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

14: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

15: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

16: / EMC_Celerra_SIDS3/ptodata/2/paa/USG96_COMB.pep:*

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14 PCT-USOS-04612-7
15 PCT-USOS-04612-7
16 US-11-056-825-7
17 USOS-1910-1964
18 US-09-80-748-1964
19 US-11-266-418-1964
19 US-11-266-418-1964
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19 US-10-535-764-184
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## APPLICANT: Felding-Habermann, Brunhilde
## APPLICANT: Janda, Kim D.
## APPLICANT: Janda, Kim D.
## APPLICANT: Saven, Alan
## TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
## TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
## FILE REFERENCE: SCRP-0043
## CURRENT APPLICATION NUMBER: PCT/USO5/04612
## CURRENT FILING DATE: 2005-02-14
## PRIOR FILING DATE: 2005-02-14
## PRIOR FILING DATE: 2006-11-10
## PRIOR FILING DATE: 2004-11-10
## PRIOR PILING DATE: 2004-11-13
## PRIOR FILING DATE: 2004-13-3
## NUMBER OF SEQ ID NOS: 13
## SEQ ID NO 2
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APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Saven, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-0042
CURRENT APPLICATION NUMBER: US/11/056,825
CURRENT FILING DATE: 2006-02-11
PRIOR PLILING DATE: 2006-11-10
PRIOR PLILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 2.
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US-11-056-825-2
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APPLICANT: Pelding-Habermann, Brunhilde
APPLICANT: Belding-Habermann, Brunhilde
APPLICANT: Belding-Habermann, Brunhilde
APPLICANT: Belding-Habermann, Brunhilde
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
TILE REFERENCE: SCRP-0043
CURRENT APPLICATION NUMBER: PCT/USO5/04612
CURRENT FILING DATE: 2005-02-14
PRIOR PILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR PILING DATE: 2004-11-10
PRIOR PELING DATE: 2004-11-10
PRIOR PELING DATE: 2004-11-13
PRIOR PELING DATE: 2004-13-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Version 3.3
SEQ ID NO 7
LENGTH: 259
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   DB 40; Length 261;
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100.0%; Score 1398; DB 40, 100.0%; Pred. No. 2.7e-107,
                                                         0; Mismatches
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                                                         261; Conservative
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                               Similarity
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RESULT 6
PCT-US02-36496-1964
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                                                                                                                                                                   APPLICANT: Janda, Kim D.
APPLICANT: Janda, Kim D.
APPLICANT: Saven, Alan
TITLE OF INVENTION METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
PILE REPERBUCE: SCRP-0042
CURRENT APPLICATION NUMBER: US/11/056,825
CURRENT PILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/544,807
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ. 1D NOS: 13
SOFTWARE: Patentin version 3.3
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
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Pred. No. 5.6e-106;
0; Mismatches 1;
                                                                                                      Sequence 7, Application US/11056825
; GENERAL INFORMATION:
; APPLICANT: Felding-Habermann, Brunhilde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic Construct US-11-056-825-7
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Best Local Similarity 99.6%;
Matches 258; Conservative
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                                                                                    US-11-056-825-7
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121 VSSGGGGGGGGGGGGGALDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW 180
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PPS23PCT2
CURRENT APPLICATION NUMBER: PCT/US02/36496
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/31,469
PRIOR PLING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PLING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1964
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                                                                                                                                                                                                                                        Query Match 81.2%; Score 1135; DB 1; Best Local Similarity 86.2%; Pred. No. 1.8e-85; Matches 219; Conservative 15; Mismatches 10;
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86.2%; Pred. No. 1.8e-85;
vative 15; Mismatches 10;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1964
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Best Local Similarity 86.24
Matches 219; Conservative
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PCT-US01-19110-1964
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PCT-US02-36496-1964
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US-11-054-515-1964
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GENERAL INVENTALIANS

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFREENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-61-15

PRIOR PILING DATE: 2000-61-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN NUMBER: 60/293,499

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN OF SEQ ID NOS: 3239

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GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: 06/331,469
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-19
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-615
PRIOR PLING DATE: 2001-615
PRIOR PLING DATE: 2001-615
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Best Local Similarity 86.2%; Pred. No. 1.8e-85;
Matches 219; Conservative 15; Mismatches 10; Indels 10
                                                                                                                                                                            ; Sequence 1964, Application US/09880748; GENERAL INFORMATION:
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                          240 PFTFGQGTKMEIKR 253
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234 PRIFGQGTKVEIKR 247
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ORGANISM: Homo sapiens
US-09-880-748-1964
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61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDE-----PYWGQGTLVT 115
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JEGURAL INFORMATION:

GENERAL INFORMATION:

JAPPILGANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P3

FURRENT PILING DATE: 2005-02-10

PRIOR PILING DATE: 2004-02-11

PRIOR PLILING DATE: 2004-06-18

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2000-11-16

PRIOR PILING DATE: 2001-11-16

PRIOR PLILING DATE: 2001-11-16

PRIOR PLILING DATE: 2001-11-16

PRIOR PLILING DATE: 2001-12-19

PRIOR PLILING DATE: 2001-12-19

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-06-25

PRIOR PLILING DATE: 2001-06-25

PRIOR PLILING DATE: 2001-06-25

PRIOR PLILING DATE: 2001-06-25

PRIOR PLILING DATE: 2001-06-25

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-21

PRIOR PLILING DATE: 2001-03-31

PRIOR PLILING DATE: 2001-03-31

PRIOR PLILING DATE: 2001-03-31

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PRIOR PLILING DATE: 2001-03-31

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86.2%; Pred. No. 1.8e-85;
ative 15; Mismatches 10;
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/26,248
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-16-16
PRIOR FILING DATE: 2000-06-16
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Best Local Similarity 86.2%
Matches 219; Conservative
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US-10-293-418-1964
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Sequence 1964, Application US/60725626
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulaton
FILE REFERENCE: PF523PP8
CURRENT APPLICATION NUMBER: US/60/725,626
CURRENT APPLICATION DATE: 2005-10-13
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1964
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator FITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator FILE REPRENCE: PF523PP9
CURRENT APPLICATION NUMBER: US/60/735,988
CURRENT APPLICATION DATE: 2005-11-14
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1964
  121 VSSGGGGGGGGGGGGALDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW 180
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                                                                                   61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARNPYYYDSSEGFFDYWGQGTMVT
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86.2%; Pred. No. 1.8e-85;
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86.2%; Pred. No. 1.8e
tive 15; Mismatches
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                                                                                                                                                          234 PRIFGOGIKVEIKR 247
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Matches 219; Conservative
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Best Local Similarity 86.2*
Matches 219; Conservative
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US-60-735-988-1964
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GENERAL INFOGRATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulate
FILE REFERENCE: PF52PD1

CURRENT APPLICATION NUMBER: US/11/266,444

CURRENT FILING DATE: 2005-11-04

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-16

PRIOR PLING DATE: 2000-06-16

PRIOR PAPLICATION NUMBER: 60/240,816

PRIOR PLING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER: PALENTING DATE: 2001-05-25

SOFTWARE: PALENTING DATE: 2001-05-25

SOFTWARE: PALENTING DATE: 2001-05-25

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                                                                                                                                                                                                                                     3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNTHY
                                                                                                                                                                                                                                                                   QVQLQQSGAEVKEPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                    Length 253;
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                                                                                                                               81.2%; Score 1135; DB 40;
86.2%; Pred. No. 1.8e-85;
ive 15; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 42;
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; Pred. No. 1.8e-85;
15; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.2%;
86.2%;
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                                                                                                                                                       Best Local Similarity 86.2
Matches 219; Conservative
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Best Local Similarity 86.23
Matches 219; Conservative
                                                ; ORGANISM: Homo sapiens
US-11-054-515-1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-266-444-1964
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LENGTH: 253
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies Against F1 and V Antigens of Yersinia Pestis FILE REPERBNCE: PF603P1
CURRENT APPLICATION NUMBER: US/10/762,593
CURRENT FILING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 1272
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSS 118
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                                                                                                                                                                                                                                                                                          72.4%; Score 1011.5; DB: 78.7%; Pred. No. 3.1e-75; Live 20; Mismatches 24
CURRENT FILING DATE: 1998-12-01
RARLIER APPLICATION NUMBER: 60/067,428
EARLIER FILING DATE: 1997-12-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
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ORGANISM: Artificial Sequence
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Matches 185; Conservative
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                                                                                                                                      LENGTH: 242
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulate
FILE REFERENCE: PF523PP10
CURRENT APPLICATION NUMBER: US/60/776,665
CURRENT PILING DATE: 2006-02-27
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1964
LENGTH: 253
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                                                                   61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDE-----PYWGQGTLVT 115
                                                                                               61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARNPYYYDSSEGFFDYWGQGTMVT 120
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VSSGGGGGGGGGGGGG--EIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSW
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Sequence 14, Application US/09202000
GENERAL INFORMATION:
APPLICANT: Sawyer, Jaymie R.
APPLICANT: Winter, Greg P.
APPLICANT: Winter, Greg P.
APPLICANT: Winter, Greg P.
TITLE OF INVENTION: COMPLEX SPECIFIC ANTIBODIES, METHOD OF TITLE OF INVENTION: COMPLEX SPECIFIC ANTIBODIES, METHOD OF TITLE OF INVENTION: UNMBER: US/09/202,000
; CURRENT APPLICATION NUMBER: US/09/202,000
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86.2%; Pred. No. 1.8e-85;
tive 15; Mismatches 10;
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Matches 219; Conservative
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; ORGANISM: Homo sapiens
US-60-776-665-1964
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236 TFGGGTKVBIKR 247 ||||||::|||| 241 TFGGGTRLBIKR 252

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Search completed: August 9, 2006, 13:26:30 Job time : 605 secs

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Sequence 1964, Application US/60814869
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulaton FILE REFERENCE: PF523PP12
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: /EMC_Celerra_SIDS3/ptodata/2/paa/PCT_NEW_COMB.pep:*
: /EMC_Celerra_SIDS3/ptodata/2/paa/US06_NEW_COMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/paa/US07_NEW_COMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/paa/US09_NEW_COMB.pep:*
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:: /EMC_Celerra_SIDS3/ptodata/2/paa/US11_NEW_COMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/paa/US11_NEW_COMB.pep:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-60-814-869-1964
US-60-814-869-1964
US-60-814-152-1964
US-60-814-152-1991
US-60-1814-152-1991
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US-60-1814-152-1991
US-60-1815-559-1238
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US-60-1815-559-62
US-60-1815-559-85
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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34; Mismatches
                                                                      Sequence 1964, Application US/60834152 GENERAL INFORMATION:
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US-60-834-152-1964
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US-60-797-351-1991
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Best Local Similarity
                                                      US-60-834-152-1964
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GENERAL INFORMATION:
GENERAL INFORMATION:
1 TILE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato;
FILE REFERENCE: PF523Pp13
CURRENT APPLICATION NUMBER: US/60/815,559
CURRENT FILING DATE: 2006-06-22
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1964
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                                                                                                                                                         Length 253;
                                                                                                                                                       81.2%; Score 1135; DB 8; Length 2:
86.2%; Pred. No. 9.2e-81;
tive 15; Mismatches 10; Indels
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CURRENT APPLICATION NUMBER: US/60/814,869
CURRENT FILING DATE: 2006-06-20
NUMBER OF SEQ ID NOS: 3247
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Matches 219; Conservative
                                                                                                                                                                         Best Local Similarity 86.2
Matches 219; Conservative
                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                          US-60-814-869-1964
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US-60-815-559-1964
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                                                      SEQ ID NO 1964
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Sequence 1991, Application US/60797351

Sequence 1991, Application US/60797351

SERBEAL IMPORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator INTER PERSONE: PF523PP1

CURRENT APPLICATION NUMBER: US/60/797,351

CURRENT APPLICATION NUMBER: US/60/797,351

CURRENT FILING DATE: 2006-05-04

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1991
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILB REFERENCE: PFS23PB14
CURRENT APPLICATION UNMER: US/60/834,152
CURRENT FILING DATE: 2006-07-31
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1964
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                                                                                                                                                                                                                                                                                                                                                                              Length 253;
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Best Local Similarity 86.2%; Pred. No. 9.2e-81;
Matches 219; Conservative 15; Mismatches 10; Indels
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Sequence 1991, Application US/60834152
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REFERENCE: PF523PP14
CURRENT APPLICATION NUMBER: US/60/834,152
CURRENT FILING DATE: 2006-07-31
SUMBER OF SEQ ID NOS: 3247
LENGTH: 244
                                                                 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSSGG 120
                                                                                         61 ADSVKGRPTISRDNAKONSLYLQMNSLRAEDTAVYYCARVHSSGS---WGQGTLVTVSSGG 117
                                                                                                                                                 GGSGGGGGGGGG--EIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRP 178
                                                                                                                                                                       GOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFG 238
                                                                                                                                                                                                                                                           178 GOSPRELIYKVSNRDFGVPDRFSGSGSGTYFTLKISRVEAEDVGVYYCMQGTH--RITFG 235
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Sequence 3, Application US/11177495
GENERAL INFORMATION:
BAPPLICANT: RAPPAPORT FAMILY INSTITUTE FOR RESEARCH
TITLE OF INVENTION: METHODS OF DETECTING HAPTOGLOBIN PHENOTYPE
FILE REFERENCE: P-7018-US
CURRENT APPLICATION NUMBER: US/11/177,495
CURRENT FILING DATE: 2005-07-11
PRIOR APPLICATION NUMBER: USP 60/586,733
PRIOR PILING DATE: 2004-07-12
NUMBER OF SEQ ID NOS: 6
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; Pred. No. 1.8e-64;
34; Mismatches 29
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71.1%;
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Best Local Similarity 71.1*
Matches 177; Conservative
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US-60-834-152-1991
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OP INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulate FILE REFERENCE: PF532PP12
CURRENT APPLICATION NUMBER: US/60/814,869
CURRENT APPLICATION NUMBER: US/60/814,869
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1991
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulatc
FILE REFERENCE: PF523PP13
CURRENT APPLICATION NUMBER: US/60/815,559
CURRENT FILING DATE: 2006-06-22
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1991
LENGTH: 244
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                                                                     GQSPRRLIYKVSNRDFGVPDRFSGSGGTYFTLKISRVEAEDVGVYYCMQCTH--RITFG 235
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    GGSGGGGGGGGALDVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNWFQQRP 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.1%; Score 924.5; DB 8 71.1%; Pred. No. 1.8e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Mismatches
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Matches 177; Conservative
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Matches 177; Conservative
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QGTRLEIKR 244
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236 OGTRLEIKR 244
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; ORGANISM: Homo sapiens
US-60-815-559-1991
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                                                                                                                                QGTKVEIKR
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US-60-815-559-1991
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US-60-815-559-1238
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato FILE REFERENCE: PF523PP11
CURRENT APPLICATION NUMBER: US/60/797,351
CURRENT APPLICATION OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST OR STOREST OF STOREST OF STOREST OF STOREST OF STOREST OF STOREST 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSSGGGGGGGGGGGGGGGGGTIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQ 175
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                                                                                                                                                                                                                                DB 7; Length 277;
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                                                                                                                                                                                                                             65.8%; Score 919.5; DB 7; Length 69.4%; Pred. No. 4.9e-64; ive 39; Mismatches 29; Indels
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GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.4<sup>†</sup>
Matches 175; Conservative
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CORGANISM: Homo sapiens
US-60-797-351-1238
                                                                                               TYPE: PRT
ORGANISM: Human
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US-60-797-351-1238
                                                                                                                                                               US-11-177-495-3
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                              ID NO 3
                                                                LENGTH:
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Sequence 1238, Application US/60815559
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Attibodies that Immunospecifically Bind to B Lymphocyte Stimulaton:
FILE REFERENCE: PF523PP13
CURRENT APPLICATION NUMBER: US/60/815,559
CURRENT FILING DATE: 2006-06-22
NUMBER OF SEQ ID NOS: 3247
Sequence 1238, Application US/60814869
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REFERENCE: PF523PP12
CURRENT APPLICATION UNMERR: US/60/814,869
CURRENT FILING DATE: 2006-06-20
NUMBER OF SEQ ID NOS: 3247
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                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
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64.8%; Score 906; DB 8;
Best Local Similarity 67.7%; Pred. No. 4.9e-63;
Matches 178; Conservative 29; Mismatches 26
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Matches 178; Conservative
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US-60-814-869-1238
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REPERENCE: PF523PP12
CURRENT APPLICATION: AND SERVICE: 18/60/814,869
CURRENT FILING DATE: 2006-06-20
NUMBER OF SEQ ID NOS: 3247
                      ---DPRGDDEPY----WGQ 110
                                             61 AQKLQGRVTWTTDTSTSTAYMELRSLRSDDTAVYYCARVTSLYSSSSGGYYYYGMDVWGR 120
                                                                                                 GTLVTVSSGGGGGGGGGGGGGETVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTY 170
                                                                                                                                                                               171 LSWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGGTDFTLKISRVEAEDIGVYYCMQGT 230
                                                                                                                                                                                                      61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----DPRGDDEPY----WGQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 GTLVTVSSGGGGGGGGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTY 170
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                                                                                                                           61 AQKLQGRVTMTTDTSTSTSTAYMELRSLRSDDTAVYYCARVTSLYSSSSGGYYYYGMDVWGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 LSWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.3%; Score 899; DB 8; Length 25
68.9%; Pred. No. 1.7e-62;
iive 27; Mismatches 35; Indels
                      AQKFQGRVTMTTDTSTAYMELRSLRSDDTAVYYCAR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: August 9, 2006, 13:27:10 Job time : 35 secs
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1921, Application US/60814869; GENERAL INFORMATION:
                                                                                                                                                                                                                                                               231 HWPPRTFGQGTKVEIKR 247
                                                                                                                                                                                                                                                                                    : | ||| |||:|||||
236 DY-PLTFGGGTKLEIKR 251
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Best Local Similarity 68.9%
Matches 177; Conservative
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US-60-814-869-1921
                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-60-814-869-1921
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato FILE REFERENCE: PF523PP14
CURRENT APPLICATION NUMBER: US/60/834,152
CURRENT FILING DATE: 2006-07-31
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1921, Application US/60797351
GENERAL INFORMATION:
BPELICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato FILE REFERENCE: PF523Ppl1
CURRENT APPLICATION NUMBER: US/60/797,351
CURRENT PILING DATE: 2006-05-04
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1921
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AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPY------ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQKFQGRVTMTTDASTSTAYMELRSLRSDDTAVYYCAR------PYYDPLTAYTFQYFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 -WGQGTLVTVSSGGGGSGGGGSGGGGS--EIVLTQSPLSLPVTLGQPASISCRSSQNLVY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDGNTYLSWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYSFSSHGISWVRQAPGQGLEWVGWSSAHDDNTKY 60
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68.9%; Pred. No. 1.7e-62;
tive 27; Mismatches 35;
                                                                                                     229 YCQQYNNWPPITFGQGTRLEIKR 251
                                                                                YCMOGTHWPPRIFGQGTKVEIKR 247
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                                                                                                                                                                                                                ; Sequence 1238, Application US/60834152; GENERAL INFORMATION:
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Best Local Similarity 68.9
Matches 177; Conservative
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CRGANISM: Homo sapiens
US-60-834-152-1238
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; ORGANISM: Homo sapiens
US-60-797-351-1921
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US-60-797-351-1921
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us-11-056-825-2.rpr

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

August 9, 2006, 13:09:51; Search time 40 Seconds (without alignments) 627.814 Million cell updates/sec

US-11-056-825-2 1398 1 MAQVQLVQSGAEVKKPGASV......KVEIKRGLGGLVDYKDDDDK 261

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	single chain Fv an	g heavy cha	J.	g kappa cha	מ	g kappa chain	chain	g kappa	g kappa chain	kappa chain	g kappa	Ig kappa chain V r	VK pro		kappa	anti-PR2 erythrocy	kappa	kappa chain V		kappa chain -	heavy	kappa chain -	heavy chain V	heavy	i-Sm antibody	heavy chain V	g heavy	kappa chain -	
SUMMARIES	ŒĨ	S41374	A56446	JC5322	B49002	S49572	S23230	K2HURP	S22658	A24452	S40324	\$40338	S22902	S42611	S40374	S40322	PL0105	S42268	S42267	836271	S40376	S36260	840312	1966	3626	953	32	6817	S40373	~
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	Query Match Length	249	268	233	114	114	133	133	140	133	133	122	142	133	118	132	160	120	120	122	134	129	126	124	118	135	142	125	128	219
d	Query Match	57.8	48.4	47.2	ö	40.2	40.2	40.1	39.6	39.5	39.4	39.4	39.5	39.1	38.3	37.9	37.3	37.3	36.7	36.4	36.3	36.2	35.9	35.5	34.8	34.8	34.2	33.9	33.7	33.7
	Score	808	6.979	099	595	562	561.5	560.5	553	552.5	551.5	520.5	547.5	546.5	535.5	529.5	521.5	521	513	509.5	507	505.5	501.5	496	487	486	478.5	473.5	471.5	471.5
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R.Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A,Title. A high affinity digoxin-binding protein displayed on M13 is functionally identic
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Recession: A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan.1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: As6446

Ig heavy chain V r Ig heavy chain V r	Ig kappa chain V-I Ig kappa chain (mo	Ig kappa chain V r Ig light chain V r	Ig kappa chain pre Ig heavy chain V r	Ig kappa chain - h anti-DNA autoantib	Ig light chain pre Ig kappa chain V r	Ig kappa chain V r anti-digoxin trans	Ig kappa chain - h antibody Fab Jel 1
S26919 S31600	C34153 PC4203	S15673 S38719	D29380 S31596	S40355 PL0203	B39276 S38715	PT0359 PH0106	S40342 S53750
0 0	01 01	0 0	77	7 7	77	0 0	0 0
98 136	101	111	131	131	131 115	118	135
33.7	33.5 33.4	33.3 33.3	33.3 33.3	33.2	33.2 33.1	33.1	33.1 33.0
471	469 466.5	465.5	465.5 465	464 463.5	463.5	462.5	462.5
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ALIGNMENTS

2006

15:56:48

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Aug

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A; Residues: 1-233 <JAN>
A; Cross-references: UNIPARC:UPI000017C2DE
A; Experimental source: hydricloma cell
C; Comment: This protein specifically binds the tumor suppressor protein p53. It restores
                                                                                                                                                                                 'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53 specific single-chain antibody Pab421 - human (5)Species: Homo sapiens (man) (5)Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997 (5)Accession: JC5322 R;Jannot, C.B.; Hynes, N.E. R;Jannot, C.B.; Hynes, Res. Commun. 230, 242-246, 1997 A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53. A;Reference number: JC5322; MUID:97168950; PMID:9016757
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                                                                                                                                                                                                                                                                                                                  HYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                        GGGGSGGGGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGSGGGDSGGGGSDIELTQSPAIMSASLGEKVTMSCRASSSV-----NPIYWYQQKS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DASPKLWVYYTSHLPPGVPARFSGSGSGNSYSLTISSMEGEDAATYYCQQFTS-SPFTFG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGSGGGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQSPRRL 185
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                                                                                                                                                                                                                                                      1 MAQVKLQESGAELVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGIT
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Ç;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 47.2%; Score 660; DB 2; Length 233; Best Local Similarity 58.3%; Pred. No. 2.3e-39; Matches 140; Conservative 33; Mismatches 57; Indels 10;
                                                                                                                                                                                 6
                                                                                                                                   Length 268;
                                                                                                                                                                                 68; Indels
                                                                                                                                     DB 2;
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 cTAN>
A;Cross-references: UNIPAC:UPI000017C6D0; GB:U20617
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                   48.4%; Score 676.5; DB 2 54.6%; Pred. No. 1.9e-40; iive 36; Mismatches 68
                                                                                                                                                          Best Local Similarity 54.6
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OGTKVEIKR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 SGTKLEIKR 242
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                                                                                                                                     Query Match
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C;Species: Homo sapiens (man)
C;Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C;Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C;Accession: 849572
Siachino, C.; Padovan, E.; Lanzavecchia, A.
submitted to the EMBL Data Library, November 1994
A;Description: k+l+ dual receptor B cells are present in the human peripheral repertoire.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Exp. Med. 173, 1033-1036, 1991
A;Title: Nevel chromosome translocation caused by fusion of immunoglobulin heavy and ligh A;Reference number: S23230; MUID:91178438; PMID:1840606
A;Accession: S23230
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                                                                                                             and V kappa II gene
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A;Cross-references: UNIPARC:UP10000116709; EMBL:246626; NID:g575261; PIDN:CAA86596.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>
                                                      Koopman, W.J.; Schroeder, H.W.J.; Gaskin,
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23230
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                            A, Experimental source: EBV-transformed lymphoblastoid cell line SSH23
A, Note: sequence inconsistent with the nucleotide translation
A, Note: sequence extracted from NCBI backbone (NCBIN:110263, NCBIP:110264)
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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                                    Ristuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, Arthritis Rheum. 35, 900-904, 1992
A;Title. A rheumatcoid factor from a normal individual encoded by VH2 A;Reference number: A49002; WUID:92352481; PMID:1322670
A;Accession: B49002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 SGVPDRFSGSGSGSTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQGTKVEIKR
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                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: Q9UL80; UNIPARC: UPI0000176B43
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Ig kappa chain precursor V-J region - human (fragment)
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Matches 102; Conservative
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Best Local Similarity 92.1
Matches 105; Conservative
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                                                                                                                                                                                                     A;Status: preliminary A;Molecule type: mRNA
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C; Genetics:

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R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acida Res. 20, 2601, 1992
A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-as
A;Reference number: S22657; MUID:92285150; PMID:1598223
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A;Cross-references: UNIPARC:UP10000113B46; GB:M36859; NID:g185932; PIDN:AAA58920.1; PID:ç
A;Note: this sequence was determined from the differentiated gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Till Kappa chain precursor V-II region (RPMI 6410) - human CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiDate: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
CiAccession: A24452
R;Weir, L.; Leder, P.
Nucleic Acids Res. 14, 3957-3970, 1986
A;Title: Structure and expression of a human subgroup II immunoglobulin kappa gene. A3;Reference number: A24452; MUID:86232631; PMID:3086847
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F:21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted
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                             Ig kappa chain precursor V region (0-81VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jan.1998 #sequence_revision 06-Feb-1998 #text_change 31-Dec-2004
C;Accession: S22658
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85.6%; Pred. No. 4.2e-32;
tive 11; Mismatches 6; Indels
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89.0%; Pred. No. 4.3e-32;
ative 6; Mismatches 6; Indels
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A,Cross-references: GDB:136265
A,Map position: 2p12-2p12
A;Introns: 17/1
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Best Local Similarity 89.03
Matches 105; Conservative
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A; Residues: 1-140 <HIR>
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                                A;Molecule type: DNA
A;Residues: 1-133 <KEN>
A;Cross-references: UNIPARC:UP10000115EA9; EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID
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C;Date: 30-Jun-1997 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Date: 30-Jun-1997 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A01890
R;Klobeck, H.G; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A;Reference number: A93588; MUID:86041852; PMID:2997711
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21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
21-43/Region: framework 1
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                      Score 561.5; DB 2; Length 133;
Pred. No. 1e-32;
8; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-133 <KLO>
A;Cross-references: UNIPROT:P06310; UNIPARC:UPI000012E159
A;Note: the sequence was determined from the differentiated gene
                                                                                                                                                                                                        C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;36-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
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Pred. No. 1.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;82-113/Region: framework 3
F;114-122/Region: complementarity-determining 3
F;123-113/Region: framework 4
F;43-113/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36-115/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.0%;
Matches 105; Conservative
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Best Local Similarity 89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: GDB:136265
A,Map position: 2p12-2p12
A,Introns: 17/1
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A;Status: preliminary
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Genetics:

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Ig kappa chain V region - human

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A;Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region usi A;Reference number: S22902; MUID:91276289; PMID:1905262
A;Accession: S22902
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J. Weuroimmunol. 36, 199-39, 1992
Affitel: NMA sequence analysis and comparison of the variable heavy and light chain regic
A;Reference number: S42610; MUID:92138794; PMID:1370957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-133 <SPA>
A;Cross-references: UNIPARC:UPI000011378B; EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-115/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 SNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQGTKVEIKR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S40374
R;Klein, R:, Jaenichen, R:; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUNVK protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 GSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNWFQQRPGQSPRRLIYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 SNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQGTKVEI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 142;
                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI0000176CAB; EMBL:X56510
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterortetramer; immunoglobulin
F;47-1126/Domain: immunoglobulin homology < NMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 547.5; DB Pred. No. 1e-31; 9; Mismatches
                                                                                                                                          A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-142 <CHA>
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87.9%;
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Best Local Similarity 87.94
Matches 102, Conservative
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40338
R;Klain, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40318
A;Recession: S40338
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C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: 84034
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Rix. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT: OBTCDO; UNIPARC: UPI0000176CAA; EMBL: X72434 C; Superfamily: immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;33-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 133;
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Pred. No. 5.4e-32;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 87.3%; Pred. No. 5.1e-32; Matches 103; Conservative 8; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.4%; Score 551.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S40324
A;Status: preliminary; translation not shown
KMolecule type: mRNA
A;Residues: 1-133 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Status: preliminary, translation not shown A, Molecule type: mRNA
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R;Chastagner, P.; Theze, J.; Zouali, M.
Gene 101, 305-306, 1991
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39.4%; 88.1%;

Conservative

190

g ð RESULT 12

Similarity

Query Match Best Local Simil Matches 104; (

A; Residues: 1-122 <KLE>

kappa chain - human

RESULT 11

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<u>.,</u>
                                                   130 GGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQSPRRLIYKV 189
                                                                  1; Gaps
  DB 2; Length 118;
                          Indels
38.3%; Score 535.5; DB 2;
85.6%; Pred. No. 5.9e-31;
tive 8; Mismatches 8;
             Best Local Similarity 85.6
Matches 101; Conservative
  Query Match
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Ig kappa chain - human

C;Species: Homo sapiens (man)
C;Accession: 6-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840322
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341

A; Status: preliminary; translation not shown

A;Cross-references: UNIPARC:UPI0000116148; EMBL:X72432; NID:g441332; PIDN:CAA51100.1; PI CS.Superfamily: immunoglobulin V region; immunoglobulin homology C;Seywords: heterotetramer; immunoglobulin homology cIAC,Seywords: heterotetramer; immunoglobulin homology cIMM> A; Molecule type: mRNA A; Residues: 1-132 < KLE>

130 GGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQSPRLIYKV 189 1; Gaps Score 529.5; DB 2; Length 132; Pred. No. 1.7e-30; 9; Mismatches 9; Indels 1 Query Match
Best Local Similarity 83.9%;
Matches 99; Conservative ઠે

1;

16 GSSGDVWMTQSPLSLPVTLGQSASISCTSSQSLVYTDGKIYLNWFQQRPGQSPRRLIFKV 75 g ò a

Search completed: August 9, 2006, 13:15:24 Job time : 41 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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	Search time 300 Seconds (without alignments)
	Search t (without
OM protein - protein search, using sw model	August 9, 2006, 13:06:26; Search time 300 Seconds (without alignments)
OM protein -	Run on:

Title:
US-11-056-825-2
Perfect score: 1398
Sequence: 1 MAQVQLVQSGABVKKPGASV.....KVEIKRGLGGLVDYKDDDDK 261

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 2849598 segs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

														-													_						_
		Description	Q65zc8 homo sapien	Q65zq7 mus sp. b3(Q65zc9 homo sapien		Q921a6 mus musculu	Q65zl2 mus sp. fv/	mus	рошо	homo	Q8tcd0 homo sapien	Q6p491 homo sapien	homo	homo	homo	Q5f2i0 mus musculu	Q8nek0 homo sapien	Q9u192 homo sapien	Q9u195 homo sapien	mus n	homo	P06309 homo sapien	mus o	Qépihé homo sapien	homod	homo	P01617 homo sapien	mus n	рошо	hom	265zc0 mus musculu
		De	90	8	90	90	07	6	90	60	60	PO	87	90	90	07	90	50	8	6	60	PO	60	Po	50	90	P0	90	P0	60	60	8	90
SUMMARIES		ΙD	Q65ZC8 HUMAN	Q652Q7_9MURI	Q6KB05 MOUSE	Q652C9 HUMAN	Q7TQM2 MOUSE	Q921A6 MOUSE	Q65ZL2_9MURI	Q925S1 MOUSE	Q9UL80 HUMAN	KV2F HUMAN	Q8TCD0 HUMAN	Q6P491 HUMAN	Q6N091_HUMAN	Q727P5_HUMAN	Q6N030 HUMAN	Q5F210 MOUSE	OBNEKO HUMAN	Q9UL92 HUMAN	O9UL95_HUMAN	KV2G_MOUSE	Q9UL94 HUMAN	KV2E HUMAN	Q58EU8_MOUSE	Q6PIH6 HUMAN	KV2B HUMAN	Q6N041 HUMAN	KV2D HUMAN	Q925S2 MOUSE	Q9BRVO_HUMAN	O960SO_HUMAN	Q652C0_MOUSE
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		Match Length	244	248	255	240	243	241	487	218	114	133	239	239	200	469	518	115	239	124	125	113	119	117	239	240	113	498	113	170	200	159	219
	.* Ouery	Match	60.7	59.2	54.7	52.3	51.6	51.4	51.3	47.5	40.4	40.1	39.9	35.3	35.3	34.2	33.7	33.7	33.3	33.0	33.0	32.8	32.8	32.7	32.6	32.3	32.2	32.2	32.1	31.9	31.8	31.8	31.4
		Score	848.5	828	764.5	730.5	721.5	718.5	717.5	664.5	565	560.5	557.5	493.5	493.5	477.5	471.5	471	465.5	462	461.5	458.5	458.5	456.5	455.5	451	450.5	450	448.5	446	445	444	438.5
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Q6P089_HUMAN Q7Z3Y5_HUMAN KV2A_HUMAN	Q9GYZZ MOUSE HV1C HÜMAN KV2C HÜMAN HV1B HÜMAN	QSBJZZ RAT QS3VP8_MOUSE Q9UL89_HUMAN	Q8WY24 HUMAN Q5EBM2 HUMAN Q5XKG4 MOUSE
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480 86 115	119	458 112 116	497 519 234
31.0 30.6 30.5	30.2	30.00 29.9 7	29.6 29.6 4.6
433.5 428 426	425.5 425 422 421	419.5 417.5 417	414.5 414 410.5
33 33 34	3.5 3.7 3.7 3.8	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	. 4. 4. 6. 4. 7.

AL IGNMENTS

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61 AQKEQGRVTMTTDTSTSTAYMBLRSLRSDDTAVYYCARDPRGD---DEPYWGQGTLVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 SGGGGGGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SGGGGGGGGGGGGGGDIQMTQSPSTLSASIGDRVTITCRASEGIYH-----WLAWYQQK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 PGQSPRRLIYKVSNRDSGVPDRFSGSGGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTF 237
                                                                                                                                                                                                                                                                                                                                    Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                 пошо варьель (лишал).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDHYMHWYRQAPGQGLEWMGWIDPNNGDTRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI--NNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
60.7%; Score 848.5; DB 2; Length 244;
Best Local Similarity 65.6%; Pred. No. 6.1e-61;
Matches 164; Conservative 34; Mismatches 41; Indels 11
                                                                                                                                                                                                                                           MEDLINE-97362799; PubMed-9219263; DOI=10.1038/nbt0797-629; Kontermann R.E., Wing M.G., Winter G., "Complement recruitment using bispecific diabodies."; Nat. Biotechnol. 15:629-631(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 244 245 26127 MW; 4BIF17868338F2BF CRC64;
                                11-OCT-2004, integrated into UniProtKB/TrEMBL. 11-OCT-2004, sequence version 1. 1. PEB-2006, entry version 9. Single-chain Fv (Fragment).
 244 AA.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL, Y13057; CAA73500.1; -; mRNA.
InterPro; IPR001599; Ig.
InterPro; IPR00710; Ig-like.
InterPro; IPR007100; Ig-like.
InterPro; IPR0071306; V-get.
SNART; SM00409; IG; 2.
SNART; SM00409; IG; 2.
PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain.
NON TER 1
NON TER 244 244
SEQÜENCE 244 AA; 26127 MM; 4BIF1
 PRELIMINARY;
                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                             NCBI_TaxID=9606;
Q652C8_HUMAN
Q652C8;
                                                                                                         Name=scFv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSGGGGGGGGETVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VOLVOSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWINNGNTH--YA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCSGGGGGGGGSDVLMTQSPLSLPVSLGDQASISCRSSQIIVHSNGNTYLEWYLQKPGQ
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92020904; PubMed=1924323; Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.; Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.; Brinkmann U., Pastan I.; a single-chain immunotoxin that causes complete regression of a human carcinoma in mice."; Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 248;
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tive 41; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AA; 26634 MW; 7A3759B43E570950 CRC64;
                                                                                                                                                                                                                                           EMBL; S57990; AAB19971.2; -; mRNA. SMR; Q65ZQ7; 4-247.
InterPro; IPR03599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR007110; IG-like.
InterPro; IPR001396; IG.v.
InterPro; IPR013106; V-Set.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv. 2.
PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain.
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Best Local Similarity 64.2'
Matches 158; Conservative
                                                                           238 GQGTKVEIKR 247
                                                                                                                          235 GGGTKLEIKR 244
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TKLEIK 247
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RESULT 3 O6KB05_MOUSE

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118 SGGGGGGGGGGGGGGEIVLTQSPLSLPVTLGQPASISCRSSQNLVYS-DGNTYLSWFQQ 176
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Distributed under the Creative Commons Attribution-NoDerivs License
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Pubmed=1545827; DOI=10.1074/jbc.M407213200;
Pubmed=1545827; DOI=10.1074/jbc.M407213200;
Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
Briand J.P., Hoebeke J.;
Modulation of the M2 muscarinic acetylcholine receptor activity with
monoclonal anti-M2 receptor antibody fragments.";
J. Biol. Chem. 279:55697-55706(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 RPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRT
                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.7%; Score 764.5; DB 2; 59.6%; Pred. No. 4.5e-54;
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11-0CT-2004, sequence version 1.
07-FBB-2006, entry version 9.
Single-chain Fv (Fragment).
                                           05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ746180; CAG34081.1; -; Other_DNA.
                                                                 05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 11.
ScFv BBES procein (Fragment).
Name=scFv BBES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01837; IKCR.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig-like.
InterPro; IPR003100; Ig-like.
InterPro; IPR003100; V-Set.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain.
PRELIMINARY;
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Q65ZC9;
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FGAGTKLEIK 249
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  D6KB05 MOUSE
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GGSGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIY----RWLAWYQQKPGK 174
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                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                   3 OVOLVOSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGOGLEWMGWI--NNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-Igk-V33; Synonyms-scFv 6H8;
Mus musculus (Mouse)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
                                                                                                                                                                                                                                                                                                                                    DB 2; Length 240;
                                                                           MEDIJNE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629; Kontermann R.E., Wing M.G., Winter G.; "Complement recruitment using bispecific diabodies."; Nat. Biotechnol. 15:629-631(1997).
                                                                                                                                                                                                                                                                                                                           Score 730.5; DB 2; Lungared, No. 2.5e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTTQM2 MOUSE PRELIMINARY; PRT;
                                                                                                                                                              EMBL; X13056; CAA73499.1; -; mRNA
                                                                                                                                                                                LinkHub; Q65ZC9; -.
InterPro; IPR001599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR001106; V-Bet.
SMART; SM00409; IG; 2.
PROSITE; PS00406; IG; 2.
Immunoglobulin domain.
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                                                        NUCLEOTIDE SEQUENCE.
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                                NCBI_TaxID=9606;
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61 AQKFQCRVTWTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGDDEPYWGQGTLVTVSSGG 120
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                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWI - - NNGNTHY
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
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"scFv single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor.";
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NUCLEOTIDE SEQUENCE.
MEDLINE=91341411; PubMed=1908510; DOI=10.1084/jem.174.3.613;
Stark S.B., Caton A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 AA; 25976 MW; BEFFF64D2DCF4F76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.6%; Score 721.5; DB 2 56.9%; Pred. No. 1.4e-50;
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01-DEC-2001, sequence version 1.
07-EBB-2006, entry version 19.
Anti-CEA 79 single chain Fv (Fragment).
                                                                                                                                                                                                                             EMBL; AJ574851; CAE00495.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Mismatches
                                                    the beta-2 adrenergic receptor.";
J. Biol. Chem. 278:36740-36747(2003).
                                                                                                                                                                                                                                                     HSSP, P01751; 1A6W.
SMR; OTTQM2; 1-236.
MGI; MGI:96514; 1Gk-V33.
INTERPO; IPR001359; 1G.
INTERPO; IPR007110; IG-like.
INTERPO; IPR007110; IG-like.
INTERPO; IPR007110; IG-like.
INTERPO; IPR007110; IG-like.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG LIKE; 2.
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Q921A6;
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PRT;
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GGGTRLEIK 254
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STRAIN=BALB/c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 SPRRL----IYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPP-R 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNTHY 60
                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
"Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally distinct variable regions."; J. Exp. Med. 174:613-624(1991).
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mu8.
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"A genetically engineered single-gene-encoded anti-TAG72 chimeric antibody secreted from myeloma cells.";
Hum. Antibodies Hybridomas 6:161-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.4%; Score 718.5; DB 2; Length 241; 54.8%; Pred. No. 2.4e-50; ive 42; Mismatches 53; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26086 MW; 0276887248E9C771 CRC64;
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11-0CT-2004, integrated into UniProtKB/TrEMBL.
11-CCT-2004, sequence version 1.
07-FEB-2006, entry version 13.
                                                                                                                                           EMBL; U88067; AAB48044.1; -; mRNA.
PIR; S19965; S19967.
PIR; S19968; S19967.
PIR; S19968; S19968.
PIR; S26325; S26325.
HSSP; POL607; 1BWN.
INCEPTO; IPR003599; IG.
INCEPTO; IPR003599; IG.
INCEPTO; IPR003599; IG.
INCEPTO; IPR003596; IG.
INCEPTO; IPR003596; IG.
INCEPTO; IPR003596; IG.
SWART; SM00409; IG; 2.
SWART; SM00409; IG; 2.
FROSITE; PSS0335; IG LIKE; 2.
FROSITE; PSS0335; IG LIKE; 2.
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MEDLINE=96272580; PubMed=8688499;
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Best Local Similarity 54.84
Matches 138; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AA;
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SEQUENCE
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120 GGGSGGGGGGGGGTVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWPQQRPG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.3%; Score 717.5; DB 2; Length 487; 56.6%; Pred. No. 6.5e-50; ive 46; Mismatches 45; Indels 17
                                                                                    EMBL, 882493; AAB37424.2; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig.
InterPro; IPR003199; Ig.cl.
InterPro; IPR003599; Ig.cl.
InterPro; IPR0030596; Ig.cl.
InterPro; IPR013106; V=et.
InterPro; IPR013106; V=et.
InterPro; IPR013106; V=et.
Pfam; PR00469; IG; 2.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 2.
SWART; SW00406; IGv; 2.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS08395; IG LIKE; 4.
PROSITE; PS08395; IG MHC; 1.
SEQUENCE 487 AA; $\overline{5}3578 MW; C7BAB69F30555504 CRC64;
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01-DBC-2001, integrated into UniProtKB/TrEMBL
01-DBC-2001, sequence version 1.
07-FEB-2006, entry version 18.
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NCBI_TaxID=9606;
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P06310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GGGGSGGGGGGGGGGGDIVLTQSPASLAVSLGQRATISCRASES-VDNIGISFMNWFQQXP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAQVKLQQSGPELKKPGETVRISCKASGYTFTTAGMQWVQKMPGKGLKWIGWINTHSGVP 60
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Wagner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001)
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MEDLINE=92352481; PubMed=1322670; Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Stuber F., Ru S.M.; "A s.M.," "A rheumatoid factor from a normal individual encoded by VH2 and V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                          47.5%; Score 664.5; DB 2; Length 218; 57.5%; Pred. No. 5.3e-46; live 42; Mismatches 48; Indels 3
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MEDINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MW X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                               218 218 23013 MW; 527E4FA8F7982817 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 GQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVE 217
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                                                                                                         EMBL, AF240168; AAK43733.1; -; mRNA.
HSSP; P01665; 1QNZ.
INTERPO; PR003599; IG.
INTERPO; IPR007110; IG-like.
INTERPO; IPR003596; IG_V.
INTERPO; IPR013106; V-set.
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                                                                                                                                                                                                                                                 SMART; SM00409; IG; 1.
SMART; SM0406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 126; Conservative
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Q9ULBO;
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                                                                                                                                                 MEDLINE=92289816; PubMed=1601042;
Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
V kappa-J kappa coding joint.";
Eur. J. Immunol. 22:1561-1565(1992).
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 EIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQSPRLLIYKVSNRD
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distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.4%; Score 565; DB 2; Length 114; 92.1%; Pred. No. 3.2e-38; ive 6; Mismatches 3; Indels
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Ig kappa chain V-II region RPMI 6410 precursor.
Homo sapiens (Human).
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PIR; A01890; KZHURP.
HSSP; Q99M37; 1191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035034; AAD56270.1; -; mRNA.
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                                somatic mutation.";
Eur. J. Immunol. 23:391-397(1993).
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InterPro; IPR003599; IG.
InterPro; IPR003596; Ig.v.
InterPro; IPR013106; V-Set.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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PIR, S23638; S23638.
PIR, S34094; S34094.
PIR, S34095; S34095.
HSSP; P01625; 1LVE.
SWR; Q9UL80; 1-114.
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130 GGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQSPRRLIYKV 189
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,

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Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 133;
                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-2.
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                                                                                                                                                                                                                                                                           .mmunoglobulin domain; Immunoglobulin V region; Signal.
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/FTId=PRO 0000015173.
Framework-1.
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Best Local Similarity 89.8%; Pred. No. 8.8e-38;
Matches 106; Conservative 6; Mismatches 5
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01-JUN-2002, sequence version 1.
07-FBB-2006, entry version 24.
Hypothetical protein.
Home sapiens (Human).
Ensembl; ENSG0000173758; Homo sapiens.
Linkhub; P06310; ...
G0; G0:0005576; C:extracellular region; NAS.
G0; G0:0003823; F:antigen binding; NAS.
G0; G0:0006555; P:immune response; NAS.
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                                                                                                              InterPro; IPR001359; IG.
InterPro; IPR00110; IG-11ke.
InterPro; IPR00110; IG-11ke.
InterPro; IPR001306; V-8et.
Pfam; PF07686; V-8et; 1.
SMART; SM00406; IG; 1.
SMART; SM0406; IG; 1.
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Q8TCDO;
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114
123
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133 AA;
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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Eur. J. Immunol. 23:3248-3262(1993).
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Wagner S.D., Luzzatto L.;
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mephritis-associated idictype.";
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Thiebe R., Zocher I., Zachau H.G.;
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                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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239 AA; 26235 MW; FACEDC3A3B0387iD CRC64;
                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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InterPro; IPR00359; IG.
InterPro; IPR00310; IG_like.
InterPro; IPR00310; IG_like.
InterPro; IPR003306; IG_WHC.
InterPro; IPR013106; V-set.
Pfam; PF07654; C1-set; 1.
SWART; SW00409; IG; 1.
SWART; SW00406; IGv; 1.
PR0SITE; PS0835; IG_LIKE; 2.
PR0SITE; PS0835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC022362; AAH22362.1; -; mRNA.
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                                                                                                                             and mouse cDNA sequences.
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PIR; S42268; S42268.
HSSP; P01834; 1172.
SMR; Q8TCD0; 21-237.
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S34095; S34095.
S40324; S40324.
S40374; S40374.
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NUCLEOTIDE SEQUENCE.
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Gaps

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78.8%; Pred. No. 5.1e-32;

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130 GGGSEIVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLSWFQQRPGQSPRRLIYKV 189
                                                               17 GSSGDIVMTQTPLSSPVTLGQPASISCRSSESLLHSNGNTYLSWLHQRPGQPPRLLIYKI 76
                                                                                                          190 SNRDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQGTKVEIKR 247
                  93; Conservative
   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
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Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
GSSGDVWHTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNWFQQRPGQSPRRLIYKV 76
                                              SURDSGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQGTHWPPRTFGQGTKVEIKR 247
                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB-Skin;
Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 AA; 26246 MW; CD7313DDFFD358B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                             QEP491 HUMAN PRELIMINARY; PRT; 239 AA. 06P491; 06P491; 05-JUL-2004, integrated into UniprotKB/TrEMBL. 07-JUL-2004, sequence version 1. 07-FRB-2006, entry version 16. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, BC063599; AAH63599.1; -; mRNA. HSSP, P01837; 1KCU.
SWR; Q6F431; 21.237.
INTERPO: IPR003599; IG.
INTERPO: IPR003599; IG.
INTERPO: IPR003599; IG.
INTERPO: IPR003596; IG.
INTERPO: IPR003596; IG.
INTERPO: IPR003596; IG.
INTERPO: IPR003596; IG.
INTERPO: IPR003596; IG.
INTERPO: IPR003596; IG.
SWART: SW00409; IG. 1.
SWART: SW00409; IG. 1.
SWART: SW00409; IG. 1.
PROSITE; PS00290; IG. LIKE; 2.
PROSITE; PS00290; IG. MHC; UNKNOWN.1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequences.
                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                   NCBL_TaxID=9606;
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                                              190
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                                                                                                                                      HUMAN
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35.3%; Score 493.5; DB 2; Length 239;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 TVSSGGGGGGGGGGGGGGGGGGGGTVLTQSPLSLPVTLGQPASISCRSSQNLVYSDGNTYLS-- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 TVSSAS-----QDGNVVVACL 187
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 SQVQLVQSGAEVKKPGASVKVSCKASGYTFSDHSITWLRQAPGQGLEWIGWISAYSGQTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Human rectum tumor;
The German Human cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.3%; Score 493.5; DB 2; Length 500; 56.1%; Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; PO1751; 1A6W.

HSSP; PO1751; 1A6W.

INTERPO; IPR003599; 1G.

INTERPO; IPR003599; 1G.

INTERPO; IPR003597; 1G.

INTERPO; IPR003106; 1G.

INTERPO; IPR003506; 1G.

INTERPO; IPR003506; 1G.

INTERPO; IPR003506; 1G.

INTERPO; IPR003506; 1G.

SWART; SW00407; IGC1; 2.

SWART; SW00409; IG.

PROSITE; PS00350; IG.MHC; UNKNOWN 2.

PROSITE; PS00350; IG.MHC; UNKNOWN 2.

Hypothetical protein; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;
                                                                                                                                                                                                                  05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FBB-2006, entry version 12. Hypotherical protein DKPZp686C02220 (Fragment). Name-DKRZp686C02220; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BX640625; CAE45779.1; -; mRNA.
                                                                                                                                                                    PRT;
                                                                                                                                                                 QEN091_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.1%;
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Straubberg R.L., Feinged E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Boaste S.B., Bonaldo M.F., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McKernan R.J., Make J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C.Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                   01-0CT-2003, integrated into UniProtKB/TrEMBL.
01-0CT-2003, sequence version 1.
07-FEB-2006, entry version 20.
                                                                                                                                                                          469 AA.
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HSSP; P01857; 1HZH.

SMR; Q727P5; 20-469.

INTERPRO; IPR001599; 19.

INTERPO; IPR001599; 19.

INTERPO; IPR001597; 19.

INTERPO; IPR0013006; 19.

INTERPO; IPR001306; 19.

INTERPO; IPR013106; V-SET.

Pfam; PF07654; C1-SET; 3.

SMART; SM00407; IGC1; 2.

SMART; SM00407; IGC1; 2.
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                          PRT;
                                                                                                                                                               Q7Z7PS_HUMAN PRELIMINARY;
Q7Z7PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences."
188 VOCFFPOEP 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                IGHG1 protein.
Name=IGHG1;
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NiH MGC Projec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDPRGD--DEPYWGOGTLVTVSS 118
                                                                                                                     59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S., Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYGITWVRQAPGQGLEWMGWIN--NGNTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 VSSGGGGGGGGGGGGGGTVLTQSPLSLPV----TLGQPASISC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 VSSAS------TKGPSVFPLAPCSRSTSGGTAALGC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 AA; 57020 MW; 93B5F98613BF6382 CRC64;
                                                                                                                                                                                                 119 GGGGGGGGGGGGIVLTQSPLSLPVTLGQPASISC 156
                                                                                                                                                                                                                                                         -----ASTKGPSVPPLAPSSKS---TSGGTAALGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FBB-2006, entry version 14.
Name=DKFZp686I15212.
                                                                                                                                                                                                                                                                                                                                                                                                  518 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BX640724; CAE45841.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                       QEN030 HUMAN PRELIMINARY;
Q6N030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 59.98
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Rectum tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P01861; IADQ
LinkHub; Q6N030; -
InterPro; IPR00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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